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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

16; Search time 2278.89 Seconds (without alignments) 4026.354 Million cell updates/sec 8, 2005, 12:35:36 September Run on:

US-10-622-407-7 Title: Perfect score:

Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database :

genesequi980s:* genesequi990s:* genesequi2000s:* genesequi2001as:* genesequi2001as:* geneseqn2003ds:* genesegn2004as:* genesegn2004bs:* geneseqn2003cs:* geneseqn2002as:*geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aad64754 Mouse tms	Adj45751 Murine tm	Aav68046 Nucleic a	Adm46622 Mouse 7F4	Adf57550 Mouse ymk	Aad64755 Mouse tms	Adj45753 Murine tm	Aad64758 Mouse tms	Adj45757 Murine tm	Add33512 Mouse mit	Add33513 Mouse mit	Aad64753 Mouse tms	Adj45749 Murine tm	Abs69674 Novel mur	Adf57563 Mouse ymk	Aas73531 DNA encod	Adq97252 Mouse can	Acn44392 Mouse gen	Acn44012 Mouse gen	Continuation (2 of
SUMMARIES	ΙD	AAD64754	ADJ45751	AAV68046	ADM46622	ADF57550	AAD64755	ADJ45753	AAD64758	ADJ45757	ADD33512	ADD33513	AAD64753	ADJ45749	ABS69674	ADF57563	AAS73531	ADQ97252	ACN44392	ACN44012	ABD32909_1
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	% Query Match	100.0	100.0	76.3	76.3	45.8	38.8	38.8	33.2	33.2	30.0	27.9	26.6	26.6	25.3	16.3	14.3	14.0	13.3	12.4	12.1
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Abd33102 Murine ca	Adg59455 Human can	Acn44120 Mouse gen	Acn44972 Mouse gen	Acn44472 Mouse gen	Abd32824 Mouse can	Abd33446 Murine ca	Acn44012 Mouse gen	Abd33360 Murine ca	Abd33489 Murine ca	Adq97135 Mouse can	Ada02873 Mouse Dpt	Adb72611 Mouse Dpt	Adc85352 Human Sel	Adm74468 Murine ca	Adg97730 Mouse can	Adg97554 Mouse can	Continuation (7 of	Continuation (6 of	Acn44804 Mouse gen	Continuation (5 of	Abd32890 Mouse can	Acn43872 Mouse gen	Adg97143 Mouse can	Acn45180 Mouse gen
3 ABD33102	2 ADQ59455	1 ACN44120	1 ACN44972	1 ACN44472	3 ABD32824	3 ABD33446	1 ACN44012	3 ABD33360	13 ABD33489	2 ADQ97135	æ	0 ADB72611	10 ADC85352		12 ADQ97730	2 ADQ97554		ABX16390 ⁻ 5	1 ACN44804	3 ABD32909 4	3 ABD32890	1 ACN43872	2 ADQ97143	1 ACN45180
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21	22	23	24	25	56	c 27	c 58	29	c 30	c 31	32	33	34	35	c 36	37	c 38	c 39	c 40	41	42	c 43	C 44	C 45

ALIGNMENTS

Bb AAD64754 standard; cDNA; 1550 Mouse tmst2-receptor cDNA. (first entry) 11-MAR-2004 AAD64754; RESULT 1 AAD64754

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNP; sepsis; cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; mouse; gene; ss cytostatic;

Mus musculus.

13. .609
/*tag= a
/product= "Mouse tmst2 receptor protein" Location/Qualifiers Key

US6627199-B1

30-SEP-2003

07-JUL-2000; 2000US-00612033.

99US-0143063P. 09-JUL-1999;

(AMGE-) AMGEN INC.

Saris C;

WPI; 2003-874309/81.

P-PSDB; ABW02715.

New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping

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Mouse; tmst2-receptor; gene; ss; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease.
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                                 The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polymucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, uital, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor cDNA used in the exemplification
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Best Local Similarity 100.
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                                                                                                                                             CTCCACCTGTGATAAAGACCAGAATATGGTGGCTGACTGTTCTGCCACCAGCGGAA 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200
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    38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            having the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a transgenic non-human animal having the expression of 7F4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agints for the prevention and treatment of diseases including osteoporosis, obesity and diabetes. The present sequence represents the modified mouse 7F4 encoding sequence.
                                                            CGCCTCTTAAGGCCTGAGTCTGCAGGCCATGTTTAATCTACTACTTTCTCTCTGCT
          CTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCCTATATCTACAATAAAACCCTTCC
                                                CTCCTCTTAAGGCCTGAATCAGTCTGTAGGTCATGTTTAATCTACTACTTTCTCTGTGCT
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                                                                                                                                                                                                                                                                                                                           7P4 gene; Osteopathic; Anorectic; Antidiabetic;
glycolipid metabolism disorder; osteoporosis; obesity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 12; Length 1509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 7F4 gen disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1182.4; DB 12; Lengtl
Pred. No. 1.1e-279;
0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression
metabolism
CCTCTCCTTTCCCCCTCTCTTCTGGTCCTTACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transgenic non-human animal with modified screening remedies for bone or glycolipid
                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
12. .542
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; SEQ ID NO 1; 44pp; Japanese
                                                                                                                                             CCCTAACCAGAAATGCAAAA 1539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito H, Makishima
                                                                                                                                                                                                                                                                                                      Mouse 7F4 encoding sequence
                                                                                                                                                                                                                                                                             (first entry)
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Matches 1321;
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diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymkz5 receptor CDNA.
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                                                                                                                                                                                       Sequence 967 BP; 262 A; 235 C; 205 G; 265 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                          Pred. No. 1.1e-163;
0; Mismatches 91;
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                                                                                                                                                                                                                             Score 709.4;
Pred. No. 1.1
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Best Local Similarity 86.7%;
Matches 831; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mouse;
  TTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCACCTCACTGACTTCCCTTCC
                          TTAACATACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCACTGGCTTCCCTTCC
                                                                                        CCTAGCTTCTCATCCCAGGTAACCCTGCCATTTTTGGTAATGTGCCTTCTTGGTTCTT
                                                                                                                       CCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAATGTGCCTTCTTGGTTCTT
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                                                                                                                                                                                                                                                                             CTCCTCTTAAGGCCTGAATCAGTCTGTAGGTCATGTTTAATCTACTTT
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4. .534
/*tag= a
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tumor, cancer, AIDS,
leukemia, hepatitis,
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                                                                                                                                                                                                           Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNP; sepsis; cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse; splice variant; gene; ss.
             1038
                                                                                                                                                                                                                                                                                                                                                               tmst2 receptor splice variant protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
           38.8%; Score 602; DB 10; Length 702; larity 93.6%; Pred. No. 2.2e-137; Conservative 0; Mismatches 0; Indels 4.
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                                                                                                                                                                                     Mouse tmst2-receptor splice variant cDNA.
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
13. .555
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                                                                                                        standard; cDNA; 702
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Best Local Similarity
Matches 657; Conserv
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                                                                                                                                                                                                                    241 CATACTCAAGGACAATGTGAGAAGTGTCACCAGGAACATTCACAGAGAAAAGATAAC
                                                                                                                                                                                                                                                                                                                                                                              421 TTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCCAGGAA
                                                                             121 AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
                                                                                                                                                        GACGICIGITGCAAGAACIGITCIGCAGGIACATITGICAAGGCGCCCTGCGAAATCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 TGCAACTCCACAGCTAACACTGTGTGTGCAGTTCATCTGTTTCAA
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TIGGACTCGGCCATGTTTGGCTTCTTCTGCAGCTTGGTGTCCCAGTCTGAGTCGCTGGTTC

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and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is a chimeric DNA comprising mouse tmst2- receptor DNA
                                                                                                                       601 CCTTTGAGTGTGTGTAATTGTGTCCTTGTTTTCCGTATCATAAGAAGATAAAGGTTC 660
                                                                                                                                                                                                                                                                                                                                                                                                                                      cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cachex; bromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse; human; immunoglobulin Fc region; chimeric; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Mouse tmst2 receptor-human immunoglobulin Fc region fusion protein" /note= "No stop codon" /partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention relates to transmembrane decoy-receptor (tmst2) proteins
                   --ATCCCAGAAACCGGCTGTTCCTACTGTTATCA
                                               541 GCCTGGCCTATCTGAATGGTTCACAGAGATCCCAGAAACCGGCTGTTCCTACTGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                     Mouse tmst2-receptor-human immunoglobulin Fc region chimeric DNA.
                                                                                                                                                         657
                                                                                                                                                                          TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT 702
                                                                                                                                                         TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT
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1. .1197
                                                                                                                                                                                                                                                                             AAD64758 standard; DNA; 1200
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- Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                               polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), ansemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases.
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                                                                                                                                                                                                                                             Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
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                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 9; 57pp; English.
                                                                 09-JUL-1999; 99US-0143063P.
                                17-JUL-2003; 2003US-00622407
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                                                                                                                     (SARI/) SARIS C.
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                                                                                                                                                                                                                                                                                                                                                                        CTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGC
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                                                                                                                                              Gaps
and human immunoglobulin Fc region DNA. This sequence is used in the exemplification of the invention
                                                                                                                                            ö
                                                                                                   Length 1200;
                                                             Sequence 1200 BP; 293 A; 361 C; 299 G; 247 T; 0 U; 0 Other;
                                                                                                 Score 514.6; DB 10; Length
Pred. No. 7.6e-116;
0; Mismatches 19; Indels
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Best Local Similarity 96.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents cDNA encoding a murine tmst2-Fc fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1200 BP; 293 A; 361 C; 299 G; 247 T; 0 U; 0 Other;
                                                     "Murine tmst2-Fc fusion protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 514.6; DB 12;
Pred. No. 7.6e-116;
0; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 4; SEQ ID NO 13; 57pp; English.
                                                                                                                                                                                                                                                                                              09-JUL-1999; 99US-0143063P.
07-JUL-2000; 2000US-00612033.
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96.5%;
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Best Local Similarity 96.5
Matches 526; Conservative
1. .1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-224390/21.
P-PSDB; ADJ45758.
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                                                                                                                                                                                                                                                                                                                                                                                            (SARI/) SARIS C.
                                                                                                                    US2004018544-A1
                                                                                                                                                                                                                                        17-JUL-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    433
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Location/Qualifiers

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The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hydridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial biology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array consen from sequence of 994 human probes and 2046 mouse probes. An array of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of mucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining an expression profile. The array is also useful for determining an expression profile diagnostic of an energy metabolism. Condition and array of the invention is useful for related physiological condition. An array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array of the invention is useful for a faced array and array of the invention is useful for a faced array array is 
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                                                                                                                             481 GCTAACACTGTGTGCAGTTCATCTGTTTCAAATGTCGACACTCACACGCCCACCGTGC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.
                                   TGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACA 480
                                                                                         GCTAACACTGTGTGCAGTTCATCTGTTTCAAATCCCAGAAACCGGCTGTTCCTACTGTTA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species, tissue and organs of such organisms, which are useful for determining expression profiles
Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;
mitochondrial disease; oxidative phosphorylation dysfunction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse mitochondrial DNA sequence SEQ ID NO:1285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Procaccio V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 1285; 201pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oxidative stress; apoptosis; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kerstann K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-2002; 2002WO-US027886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2001; 2001US-0316323P.
31-AUG-2001; 2001CA-02356540.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD33512 standard; DNA; 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-300821/29.
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                                                                                                                                                                                                                      553 TCACC 557
                                                                                                                                                                                                                                                                                541 CCAGC 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACTCTCCACCAGCCTCCTCTAAGGCCTGAATCAGTCTGTAGGTCATGTTTAATCTAC 1444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ccacrcccccaccccrarra--caaaracrcacrcrccaccarcrrraarcrac 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56
such therapies, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The sequences shown in ADD33224-ADD32560 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO'8 295, 1174, 1213, 1700, 1728, 1730, 1905,
                                                                                                                                                                                                                                                                                                                 1025 ATTTCTTATGAGGCAAGCATTCAAACACAGGGTTATGAGGGCCAAACCAATTCAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383 AACAATTTAGATGAAGGCAAGTCCTGGTATCAGGTCCAAAAGAAACTCCAGGATGAATGGT
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                                                                                                                                                                                                                                                                                                                                                                                   1085 ACCACAGGTTAACAATTGCCCTCTGCAGCTCTGGTGGAGGCCCTCCTTGAGGTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                       ACCACAGGTTAACAATTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCCTTGAGAGTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1145 AACAATTTAGATGAAGGCAAGTCCTGGTATCAGGTCCAAAAGAAACTCAGGATGAATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCACCTC
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                                                                                                                                                                                                                                                                                 7
                                                                                                                                                                                                                                           Length 503;
                                                                                                                                                                                                             Sequence 503 BP; 150 A; 80 C; 159 G; 114 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                                                                                             Score 465.4; DB 10
Pred. No. 6.4e-104;
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                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.4 Matches 487; Conservative
                                                                                                                                                                         1906, 2408 and 2643.
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261
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                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel array comprising at least two isolated hucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleic acid molecule which is an expression product of a gene involved in mitochondrial biology. The array comprises two or more chosen from sequence of 994 human probes and 2046 mouse probes. An array of the invention is useful for determining an expression profile of a mouse or thuman sample containing mucleic acid, by contacting the array of the invention is useful for determining an expression profile. The array is also useful for determining mucleic acid, by contacting the array to produce an expression profile. The array is also useful for determining on expression profile. The array is also useful for determining an expression profile ample containing mucleic acid an expression profile of a first labelled sample containing mucleic acid. The second sample is a reference or a standard. An array is useful for actermining mitochondrial biology gene expression profiles of an emergy-metabolism. Cor determining mitochondrial biology gene expression profiles of an energy-metabolism call as human, mice and closely related species, tissue and organs of unch as human, mice and closely related species, tissue and organs of alagnostic of energy metabolism-related physiological conditions, and mutations insured physiological conditions, diagnostic of energy metabolism-related physiological conditions, closely related species, tissue and organs of pathways genes, and mutations insured physiological conditions, closely related species, tissue and organs of dentifying therapeutic agence useful for determining and/or treating such physiological conditions, ending and organism and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also onergy metabolism-related physiological conditions. Organism onergy metabolism-related physiological conditions or physiological conditions, evaluating and identifying t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 ACACTCCTTCAAATGTCCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGGAAGAACTG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGCTGCTGCTGCTGCTGCTGAATCTGCCGCTAAAATTTGCTATGCTAGAATT 140
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0; Mismatches 58
                                                                                                                                                                     Procaccio V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.9%; Score 432.2;
85.7%; Pred. No. 9.6
                                                                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1286; 201pp; English.
                                                                                                                                                                     Kerstann K,
                                                                          30-AUG-2001; 2001US-0316323P
31-AUG-2001; 2001CA-02356540
                                       30-AUG-2002; 2002WO-US027886
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                                                                                                                                                                     Levy S,
                                                                                                                                                                                                          WPI; 2003-300821/29
                                                                                                                                 (UYEM-) UNIV EMORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                     Wallace DC,
   13-MAR-2003
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                                                                                                                                                                                                                 501 TGTGTGCAGTTCATCTGTTTCAAATCCCAGAAACCGGCTGTTCCTACTGTTATCACCTTT 560
                                                           270 crccaccrerearaaaaccaaaarareereecreacrerereccaccacreaceaaa 329
210 gaagrercacccaggaacarrcacaggaaagaraargeccrecargarrergaacrrre
                                                                                                          ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC
                                                                                                                                                                     390 AIGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC
                                                                                                                                                                                                                                                                                                            -------GCTAATTGTCTTCTGTATCTGAAGAGATAAAGGTTCTACAG
                                                                                          381 ATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCCAAAATTTCCAGAATCGTGCCGCCC
                                                                                                                                                                                                                                                                             561 GAGTGTGCTAATTGTGCCGTTGTTGTCTTCCGTATCATAAGAAGATAAAGGTTCTACAG
                                                                                                                                                                                                                                                                                                                                          621 ATGTTTTCT-TAGCTTCCTTTTATTGCTATGAAGTGATACTATGGAGGCAACTCTTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Mouse tmst2 receptor protein"
/note= "No stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse tmst2-receptor cDNA from tmst2-00004-d1 clone.
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The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TMP) receptor super gene family and polymucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor cDNA used in the exemplification of the invention
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tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
                      treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 412 BP; 93 A; 104 C; 102 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 412; DB 10;
Pred. No. 7.5e-91;
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                                                                                                            5; Opp; English.
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                                                                                                            Example 1; SEQ ID NO
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                                                                chromosome mapping
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                                                                                                                                                                                                                                                                                                                                                                                                                  adult respiratory distress syndrome; ARDS; tuberculosis; viral disease
                                                                                                                                ADJ45749 standard; cDNA; 412 BP.
                                                                                                                                                                                                                                            Murine tmst2 00004-d1 cDNA.
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                       06-MAY-2004
                                                                                                                                                                     ADJ45749;
                                                                                          RESULT 13
ADJ45749
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The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-receptor cDNA clone of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
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                                                                                                                                                                         /*tag= a
/product= "Murine tmst2 00004-dl"
                                                                                                                                                                                                                                                                                                             /note= "No stop codon shown"
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                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-2004
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                                                                                  Key
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Gaps

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0; Indels

Length 415;

Score 392; DB 6; Pred. No. 6.1e-86; 0; Mismatches

25.3%;

403; Conservative

Similarity

Query Match Best Local (

Matches

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250 TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA 309

310 TITCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA 369

ADF57563 standard; cDNA; 357 BP

RESULT 15

(first entry)

12-FEB-2004

ADF57563;

TTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA

421

480

189 360

241 CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC 300

130 CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAAC

301 CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 190 CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 361 TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA

70 GACGICTGITGCAAGAACIGITCTGCAGGAAATIGICAAGGCGCCCTGCGAAATCCCC

181 GACGICTGITGCAAGAACTGITCTGCAGGIACATTTGICAAGGCGCCCTGCGAAATCCCC

240 129

69

11 APATITIGCTATGCTAG-ATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA

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The invention describes an isolated murine polynucleotide (I) comprising a contiguous stretch of at least 60 nucleotides of one of 265-677 nucleotide 891 OMNIBANK gene trapped sequences (GTS8) (S), given in the specification. The novel genes and cells are useful in functional genomic diagnostic agents and methods. (I) is useful for identifying the coding regions of the murine genome, to isolate CDNAs, genomic clones, or full-length genes/polynucleotides or homologues, heterologues, paralogues, or orthologues that are capable of hybridising to one or more of the GTSs under stringent conditions. (I) can be incorporated into a phage display system that can be used to screen for proteins, or other ligands, that care capable of binding an amino acid sequence encoded by an oligonucleotide or polynucleotide sequence in at least one of the TS sequences. (I) is useful in addressable arrays, such as gene chips, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel murine polynucleotides that individually identify novel genes into which a retroviral gene trap vector has integrated, useful in genomic analysis and in discovery, development of therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phage display system; gene chip; temporal gene expression; tissue specific gene expression; antisense inhibition; gene targeting; development disorder; cell differentiation disorder; aqing; cancer; autoimmune disease; lupus; inflammatory disorder; skin disorder; degenerative disorder; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel murine polynucleotide isolated using gene trap technology #737.
   412
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Sands AT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trapped sequence;
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                                                                                                                                                                                                                                 ABS69674 standard; DNA; 415
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(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
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Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; cancer; acquired immune deficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                                     /product= "Murine ymkz5 receptor"
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                                                                                                                                                                                         /note= "No stop codon"
                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                      11-JUL-2002; 2002US-00193616
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07-JUL-2000; 2000US-00611989
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P-PSDB; ADF57549.
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                                                                                                                      Mus musculus.
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                                                                                                   ss; gene
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                                                                                                                                         Key
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Sequence 415 BP; 119 A; 107 C; 88 G; 101 T; 0 U; 0 Other;

technology

identify and characterise temporal and tissue specific gene expression, to identify the gene of interest from many sources and for genetic manipulations such as antisense inhibition and gene targeting. Decreasing the level of expression of (1) and/or down regulating the activity of peptides or proteins encoded by (1) is useful for treating development and cell differentiation disorders, aging, cancer, autoimmune disease, lupus, inflammatory disorders, skin disorders and degenerative disorders. This sequence represents a murine cDNA isolated using gene trap

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The invention relates to transmembrane decoy receptor, ymkz5 belonging to tumour necrosis factor (TNP) receptor supergene family and nucleic acid sequences encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The
                      Novel ymkz5-receptor polypeptide useful for treating diseases such as tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence is mouse ymkz5 receptor cDNA.
                                                                                                                               Example 1; SEQ ID NO 5; 57pp; English.
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DB 12; Length 357; Query Match 16.3%; Score 253.2; DB 12; Length Best Local Similarity 87.9%; Pred. No. 6.6e-52; Matches 276; Conservative 0; Mismatches 38; Indels Sequence 357 BP; 88 A; 94 C; 80 G; 95 T; 0 U; 0 Other;

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Gaps

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81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAATTTGCTATGCTAGAATT 140 44 GITCCTCTTGCTGCTGCTGCTGAATCTGTTGCCGGTAATATTTGCTATGCCTGAATC 103 ACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTG 200 104 ATACTCCTTCAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTG 163 TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGA 260 TCCCTCAGGTACATTTGTCAAGGCGCCCTGCAAAATCCCCCATACTCAAGGACAATGTGA 223 GAAGTGTCACCCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG 320 GAAGTGTCACCCCAGGAACATTCACAGGGAAAGATAATGGCCTGCATGATTGTGAACTTTG 283 381 ATGCCAGTGCCGAA 394 141 164 261 201 224 셤 ð g 8 8 8 8 g ઠ ò

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Search completed: September 8, 2005, 17:05:21 Job time : 2283.89 secs

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1550; Conservative 0; Mismatches
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Sequence 7 from patent US 6627199.
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AC097605
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14.9 148813
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Db 1321 ATGTGCCTTCTTGGTTCTTCCTCTTTCCCCCTTTCTCTTCT	RESULT 2 AY046551 LOCUS LOCUS LOCUS DEFINITION Mus musculus TNF receptor family member SOBa ACCESSION AY046551.1 GI:18056435 KEYWORDS KEYWORDS SOURCE Nus musculus (house mouse) ORGANISM Mus musculus (house mouse) BENEATORICA: Metazoa; Chordata; Craniata; Vert Mammalia: Eutheria; Rodentia; Sciurognathi;	nd Pa ine m	May, South San Francisco, CA 94080, USA FEATURES Location/Qualifiers 11555 /organism="Mus musculus" /mol type="mRNA" / db xref="taxon:10090" / .603 / .603 / .codon start=1	/ product in receptor raming memory / protein id="MALOSO73.1" / db_xref="GI:18056436" / translation= MPEPFCSLVSSVSRWFLWRL SFRCPAGEYWSKDVCKNCSAGTFVKAPCEIPHTC CSTCDKOGNVADCSATSDRKCQCRTGLYYYDPKR ANTVCSSSVSNPRNRLFLLLSPLSVLIVSVVFRI	Query Match 99.2%; Score 1537.6; DB 10; Best Local Similarity 99.7%; Pred. No. 0; Matches 1540; Conservative 0; Mismatches 4; I	Qy 7 TGGGCARGTTTGGCTTCTTCTGCAGCTTGGTGTCCAGTCTC	Oy 67 CGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTG	Qy 127 GCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAA	QY 187 TGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCC	Oy 247 CAAGGACAAIGIGAGAGIGTCACCCAGGAACAITCACAGAC
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NPRNWLFLLMLIVFCI"
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1. Biol. Chem. 278 (7), 5444-5454 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Dctrailr1"
/note="mDcTRAILR1; binds murine TRAIL but not human TRAIL;
contains a glycosyl-phosphatidylinositol (GPI) anchor;
member of the TNFR family"
                                                                                                                                                                                                                                            AY165625 1491 bp mRNA linear ROD 19-FEB-2003
Mus musculus decoy TRAIL receptor 1 (Dctrailr1) mRNA, complete cds:
                                                                       CTTTCTCTCTCTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCCCCTCCTATCTACA 1506
                                                                                                    GTTCCTCTTGCTGCTGCTGCTGATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATC 104
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Schneider, P., Olson, D., Tardivel, A., Hofmann, K., Van Vlijmen, H., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.
Direct Submission
Submitted (16-OCT-2002) Institute of Biochemistry, University of Lausanne, Boveresess 155, Epalinges CH-1066, Switzerland
Location/Qualifiers
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llarity 90.7%; Pred. No. 4.6e-285;
Conservative 0; Mismatches 100;

    .1491
    /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"

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/chromosome="7"
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/gene="Dctrailr1"
/note="synonym: T
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AY165625.1 GI:27985587
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CTGCTCAGCCACCAGTGACCGGAA 380 AAAATTTCCAGAATCGTGCCGCCC 440 CCCCCATACTCAAGGACAATGTGA 260

	AC068006/c AC068006/c LOCUS AC068006 AC068006 AC068006 VERSION ACCESSION ACC68006.10 GI:42409607 KEYWORDS ACTSON ACC8008 SOURCE MUS musculus (house mouse) ORGANISM Mus musculus (house couse) ACC8008 CEASTON ACC8008	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. REFERENCE 1 (bases 1 to 203141) AUTHORS Birren, B., Nuabaum, C. and Lander, E. TITLE Mus musculus chromosome 7, clone RP23-6117 OUGNAL Unpublished 203141)	Birren, B., I Anderson, S., Boguslavkiy, Campopiano, R. Collymore, A. Dodge, S., Do	Howland, J. C., Illev, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lett., C., Liu, G., Locke, K., Mardonald, P., Marquis, N., Mardonald, P., Marquis, N., McCarthy, M., McEurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,	Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.H., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Asymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teffsaye, S., Theodore, J., Tirrell, A., Travers, M., Trigillo, J., Volland, M., A., Manner, D., Volland, M., A., Wanner, D., Volland, M., A., Wanner, D., Volland, M., A., Wanner, D., Volland, M., M., M., M., M., M., M., M., M., M.	Young, G. Zainoun, J., Zimmer, A. and Zody, M. TITLE Direct Submission JOURNAL Submitted (27-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA REFERENCE 3 (bases 1 to 203148) AITHORS Birren. B., Nusbaum. C., Lander. E., Abouelleil, A., Allen. N.,	Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,	Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kanter, A., Kells, C., Landers, T., Levine, R., Liud, A., Kells, C., Landers, T., Machen, C., Lindblad-Toh, K., Liu, X., Liud, A., Mabbitt, R., Machen, C., Macdean, C., Macdonald, P., Major, J., Manning, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,	Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Kise, C., Kogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubba, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.	AL RS
441 AIGTACCAAGIGTCCCCAAGGAATCCCTCTCCCCGGAATGCAACTCCAGGGGTAACAC 500		563 AFGGTGTCTGTAGCTTCTTTATTGCTGTGAAGAGAACCATGGAGGCAACTCT 617 680 TTATTTATTTTATTTTATTTTTAAGGCTAACTTGATTTGAAGCAGGCTGGCT	740 CAAAATCACAGAGATCCAGACTAAGAGAAACATTTAATTGGGACTG 799	860 GCAGACATGATGTTGGAGAAGGACTGAGATTTCTGCATCTTGATCTGCAAGCAA	854 GGAGACTGTGTGCCACACTACACATAGACATAGGAGACCTCAAAGCCTGTCCCCA 913 980 CAGTGACAAACTTCCTCCAACAAGGTCATACCTAATAATACCATTTCTTATGAGGCA 1039	1040 AGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCACACACA	1034 THGCCCTCTGCAGCTCTCGGGGGCCCTTGAGAGTAACTAACT	1220 TTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCACTGACTTCCCTTCC 1279		1334 GGCTCTTAAGGCCTGAGTCAGTCTGCAGGCCATGTTTAATCTACTACTTTCTCTGCT 1393 1460 CTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTACTACTACTAAAACCTTTC 1519

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DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Brickson, J., Farco, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagoshan, D., Hagoshan, D., Hagoshan, D., Hagoshan, D., Hagoshan, D., Hagoshan, T., Halle, W., Tilev, I., Uchan, MacLean, C., Macdonald, P., Mijor, J., Manning, J., Mathews, T., Machews, C., Macdonald, P., Major, J., Manning, J., Mathews, C., Marchews, T., Marchews, T., Marchews, T., Marchews, C., Marchews, T., March, M., Meldrim, J., Meneus, L., Mihova, T., Micol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Direct Submission

Submitted (Jol-ARP-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Feb S., 2004 Hiss sequence version replaced gi:41351575.

All repeats were identified using RepeatMasker:
Smit, A. F. A. & Green, P. (1996-1997)
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Location/Qualifiers
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Center: Whitehead Institute/MIT Center for Genome Research
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Contact: sequence_submissions@broad.mit.edu
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rolone lib="RPCI-23 Female Mouse BAC"
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Center clone name: 6_I_17
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JOURNAL
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144173 ATCACCTTTGAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGAAGAAGATAAAG 144114
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Best Local Similarity 98.1%; Pred. No. 2.9e-238;
Matches 1028; Conservative 0; Mismatches 20;
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us-10-622-407-7.rge

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nucleosome assembly protein 1-like 4 protein; Obphl gene; oxysterol binding protein; Tnfrhl gene; Tnfrh2 gene; tumor necrosis factor receptor p60 homologue 1; tumor necrosis factor receptor p60 homologue 2; tumor suppressing subtransferable candidate 5. Mus musculus domesticus (western Buropean house mouse) Bus musculus domesticus (sestern Buropean house mouse) Busaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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                                                                                                                                                                                     Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R., Lane, N., Reik, W. and Walter, J. Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73,
Berlin, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin, GERMANY
On Jan 27, 2001 this sequence version replaced gi:11191799.
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
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Hum. Mol. Genet. 9 (18), 2691-2706 (2000)
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Revised by author 22-MAY-2000
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                                                                                       SOURCE
ORGANISM
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REFERENCE
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AUTHORS
TITLE
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                                                                                         TCTTTATTTTATTTATTTATTTTATTTTTAATGTCTTGAACTTGATTTGAAGACCAG
                                                                                                                                                                           GCTGGCCTCAAAATCACAGAGATCCAGACTAAGACAACTCTAATAAGGGAAACATTTAAT
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AJ276505.
AJ276502. GI:12583595
CarS gene; Cdknic gene; cyclin-dependent kinase inhibitor 1C;
cysteinyl-tRNA-synthetase; IPL gene; Itm gene; Napl14 gene;
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SNRKCJGFOGSSITAKSKFVONSLSALLDGYKALTFLNKREBYTLTMPYAHCRGILYG
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DRDVFTKEESSGGTELWTPSEEVRQQLKRHYVLLEBGSELESETLWQHYTRAIREG
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//gene="Obphl"

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48531. .48580)
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77140. .77213,77826. .77868,78677. .78828)
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join(30593. .130688,131306. .131403,132305. .132456,
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Best Local Similarity 98.1%; Pred. No. 2.9e-238;
Matches 1028; Conservative 0; Mismatches 20;
                                                                                                                                                                                                                             /gene="Cars"
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/organism="Mus musculus"
/mol type="mRNA"
/strain="NIH Swiss"
/db xref="taxon:10090"
/chTomosome="7"
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 691)
Schneider,P., Olson,D., Tardivel,A., Browning,B., Lugovskoy,A.,
Gong,D., Dobles,M., Hertig,S., Hofmann,K., Van Vlijmen,H.,
Hsu,Y.-M., Burkly,L., Tschopp,J. and Zheng,T.S.
Identification of a New Murine Tumor Necrosis Factor Receptor Locus
That Contains Two Novel Murine Receptors for Tumor Necrosis
Bactor-related Apoptosis-inducing Ligand (TRAIL)
J. Biol. Chem. 278 (7), 5444-5454 (2003)
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                                                                                                                                                                                                                                                                                                                                          /gene="Dctrailr2"
/note="synonym: Tnfrh2"
31. .627
/gene="Dctrailr2"
/note="mDcTRAILR2L; binds both murine and human TRAIL;
membrane-bound form; member of the TNFR family;
alternatively spliced"
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                       Lugovskoy, A.,
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2 (bases 1 to 691)
Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovsko)
Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovsko)
Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H.,
Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.
Direct Submission
Submitted (16-OCT-2002) Institute of Biochemistry, University and Location/Qualifiers
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38.8%; Score 602; DB 6; Length 702;
Best Local Similarity 93.6%; Pred. No. 1e-136;
Matches 657; Conservative 0; Mismatches 0; Indels
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/organism="unknown"
/mol_type="genomic DNA"
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Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL)
1246628
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                 601 AGAAGATAAAGGTTCTACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGATACT 660
                                                                                             Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 736)
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Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.
Direct Submission
Submitted (16-007-2002) Institute of Biochemistry, University of Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland
Location/Qualifiers
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TTCCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATA
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/mol type="mRNA"
/strain="NIH Swiss"
/db_xref="taxon:10090"
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/gene="Dctrailr2"
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                                                                                                                                   121 CTAGAATTACACTCCTTCAAATGTCCCGGTGAATAACTGGTCTAAAGACGTCTGTTGC
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                                                                     61 CIGCTGCTGCTGCTGCTGCTGCTGCTGTAAATTTGCTATG
AIGTTTGGCTTCTTCTGCAGCTTGGTGTCCCAGTCTGAGTCGCTGGTTCCTTTGGCGGCGG
                                                                                                                     133 CTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGC
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Unknown.
Unclassified.
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Saris,C.
Isolation, identification and characterization of tmst2, a novel member of the TYP-A-receptor Supergene family
Patent: US 6627199-A 13 30-SEP-2003;
Location/Qualifiers
1. .1200
1. .1200
                                                       CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCTTGCAGGTA
                                                                                                                                                                                         GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCC
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   TTGCACTCGGCCATGTTTGGCTTCTTCTGCAGCTTGGTGTCCAGTCTGAGTCGCTGGTTC
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rmuz/8265 669 bp mRNA linear ROD 06-MAR-2002
Mus musculus domesticus mRNA for tumor necrosis factor receptor p60
homologue 2 (Infrh2 gene).
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Submitted (30-MAY-2000) Engemann S., Department Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GBRMANY
                                                                                                                               AJ278265.
AJ278265.1 GI:11191811
Third gene; tumor necrosis factor receptor p60 homologue 2.
Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                          Engemann, S., Strodicke, M., Paulsen, M., Franck, O., Reinhardt, R., Lane, N., Reik, W. and Walter, J. Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus domesticus"
/mol_type="mRNA"
/sub_species="domesticus"
/db_xref="taxon:10092"
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Hum. Mol. Genet. 9 (18), 2691-2706 (2000)
20519229
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                                                                                                                                                                                                                                                                                                                                               /db_xref="GOA:Q9ER62"
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RPCTKCPQGIPVLQECNSTANTVCSSSVSRRSASVAWPI"
                                                                                                                                                                                                                   /product="tumor necrosis factor receptor p60 homologue 2" /protein id="CACI6406.1" /db_xref="GI:11191812" /db_xref="GO:09ER62" /db_xref
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 GCCCTGCGAAATCCCCCATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCAC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 AGAGAAAGATAACTTGGATGCTTGTATACTTTGCTCCACCTGTGATAAGATCAGGA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGAGTCGCTGGTTCCTTTGGCGGCGGCTGCTGCTG-TGCTGNTGTG--TTGTTAAT 57
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chromosome="7"
                                                                 gene="Tnfrh2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center: Cade: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: ngsc-help@bcm.tmc.edu
Center project name: CH230-229H15
Center clone name: CH230-229H15
Center clone name: CH230-229H15
Center clone name: Phrap; version 0.990329
Consensus quality: 228934 bases at least Q40
Consensus quality: 2328934 bases at least Q30
Consensus quality: 231348 bases at least Q20
Consensus quality: 231348 bases at least Q20
Consensus quality: 231348 bases at least Q20
Consensus quality: 231348 bases is least Q20
Estimated insert size: 233648; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23603435.
The sequence in this assembly is a combination of Bake based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs acaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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    .240262
    /organism="Rattus norvegicus"

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/note="wgs_end_extension
clone_end:Sp6"
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clone_end:T7"
1528. ... 3304
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/db_xref="taxon:10116"
/clone="CH230-229H15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    end_sequence:BZ111010"
complement(232905. .23.
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/note="clone_boundary
clone_end:T7
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112477

---TTTTTTAATGTCTTGAAC

112180

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----CCAGGTAAC

------ACCTCACCTT

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/product="tumor necrosis factor receptor p60 homologue 1"
/protein id="CAC16405.1"
/brotein id="CAC16405.1"
/db_xref="d0A.199R63"
/db_xref="d0A.199R63"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           561 GAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGAAGATAAAGGTTCTACAG 620
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                                                                                                                                                                                       Submitted (30-MAY-2000) Engemann S., Department Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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Lane, N., Reik, W. and Walter, J.
Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAATTTGCTATGCTAGAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 569;
                                                                                                                                                                                                                                                                                  /organism="Mus musculus domesticus"
/mol type="mRNA"
/sub_species="domesticus"
/db_xref="taxon:10092"
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                                                                     Hum. Mol. Genet. 9 (18), 2691-2706 (2000)
20519229
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Best Local Similarity 85.9%; Pred. No. 4.2e-89;
Matches 487; Conservative 0; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=experimental
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               /chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                           /gene="Tnfrh1"
79. .522
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Tnfrh1"
/codon_start=1
                                                                                                                                    (bases 1 to 569)
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Engemann, S.
Direct Submission
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Infrhl gene; tumor necrosis factor receptor p60 homologue 1.
Infrhl gene; tumor necrosis factor receptor p60 homologue 1.
Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                     111715 GGCGGTGTTCTCCCTCCTATCTACAATAAAAACCTTCCCCCTAACCATAATTGGA 111661
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   GGCTGAGCTCTCCCTCCTATTCTACAATAAAACCCTTCCCCCTAACCAGAAATGCA 1536
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Mus musculus TNF receptor family member SOB mRNA, complete cds.
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/protein id="AALO5072.1"
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/tb_xref="G1:18056434"
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VADCSATSDRKVERQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSSVS
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Ann,G., Mao,W. and Risser,P.
Characterization of SOB, a member of the TNFR family Unpublished
Cases 1 to 531)
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Submitted (18-JUL-2001) Molecular Oncology, Genentech, Inc, 1 DNA
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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                                                           621 ATGTTTCT-TAGCTTCCTTTTATTGC 646
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-18-05-18-18-18
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2224 4 US-10-116-260-44 Sequence 44, Appl 2224 4 US-10-115-671-44 Sequence 44, Appl 2224 4 US-10-115-671-44 Sequence 47, Appl 2462 4 US-09-224-364A-48 Sequence 48, Appl 2462 4 US-10-115-415-48 Sequence 48, Appl 2462 4 US-10-115-671-48 Sequence 48, Appl 2462 4 US-10-115-671-48 Sequence 48, Appl 1022 4 US-09-949-016-11852 Sequence 11852, A DIO22 4 US-09-949-016-14166 Sequence 11852, A DIO22 4 US-09-949-016-14166 Sequence 14166, A DIO24 4 US-09-949-016-14164 Sequence 44973, A DIO24 4 US-09-949-016-1400 Sequence 13032, A DIO25 4 US-09-949-016-13032 Sequence 13032, A DIO26 3 US-09-245-016-13032 Sequence 13032, A DIO26 3 US-09-245-016-13032 Sequence 5, Appli 10050 4 US-09-358-0558-5 Sequence 5, Appli	ULT 1 09-612-033B-7 equence 7, Application US/09612033B atent No. 6627199 ENERAL INFORMATION: APPLICANT: Saris, Chris APPLICANTION: Insolation, Identification, and Characterization of TITLE OF INVENTION: 1801ation, Identification, and Characterization of TITLE OF INVENTION: 0f Genes SAROR APPLICATION NUMBER: US 60/143,063 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 LENGTH: 1550 TYPE: DA ORGANISM: Mus musculus FRATURE: NAME/KEY: CDS 10-0718R INPORMATION: mouse tmst2 09-612-033B-7	100.0%; Score 1550; DB 4; Length 1550; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels 0; Gaps 0;
C 30 47.6 3.1 2224 C 31 47.6 3.1 2462 C 33 47.6 3.1 2462 C 34 47.6 3.1 2462 C 35 47.6 3.1 2462 C 36 47.4 3.1 321022 C 39 47.2 3.0 601 C 40 47.2 3.0 601 C 41 47.2 3.0 601 C 42 47.2 3.0 6551 C 43 46 3.0 90050 C 45 46 3.0 90050	RESULT 1 US-09-612-033B-7 US-09-612-033B-7 Sequence 7, Application US/09612033B Patent No. 6627199 TITLE OF INVENTION: Isolation, Identificat TITLE OF INVENTION: Isolation, Identificat TITLE OF INVENTION: Of Genes FILE REPERENCE: 01017/35434 CURRENT PILING DATE: 2000-07-07 PRIOR APPLICATION NUMBER: US/09/612,033B CURRENT FILING DATE: 1999-07-09 NUMBER OF SEQ ID NOS: 15 SOFTWARE: PatentIN Ver. 2.0 LENGTH: 1550 TYPE: DNA ORGANISM: Mus musculus FRATURE: NAMMEKEY: CDS LOCATION: (13). (606) OTHER INFORMATION: mouse tmst2	Query Match Best Local Similarity 100 Matches 1550; Conservative

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US-09-411-722-3

US-09-411-722-3

Sequence 3, Application US/09411722

Patent No. 6271366

GENERAL INFORMATION:
APPLICANT: Kimura, Nacki
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PRO'S
FILE REPERENCE: 06501/04001
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: DF 9/099653
PRIOR PILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
SOFTWARE FASEL DE NOS: 12

NUMBER OF SEQ ID NOS: 12

SOFTWARE FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Mus musculus
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RESULT 3 US-09-855-266A-3 ; Sequence 3, Application US/09855266A

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TYPE: DNA
ORGANISM: Mus musculus
FRATURE:
FRAKEY: CDS
LOCATION: (13)..(552)
OTHER INFORMATION: Primer 2086-39
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US-09-612-033B-13
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Patent No. 6627199
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Lealation, Identification, and Characterization of
TITLE OF INVENTION: Leglate, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: of Genes
FILE REFERENCE: 01017/35434A
CURRENT FILING DATE: 2000-07-07
PRIOR PAPLICATION NUMBER: US 60/143,063
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
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            GCTTACAGTTTCGGACGTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAA 859
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Sequence 13, Application US/09612033B
Sequence 13, Application US/09612033B
Patent No. 6627199
APPLICANT: Saris, Chris
ITILE OF INVENTION: Isolation, Identification, and Characterization of TITLE OF INVENTION: match, and Characterization of TITLE OF INVENTION: case, a No. 6627199el Member of the TNF-Receptor Superfamily TITLE OF INVENTION: case, and Characterization of TITLE OF INVENTION: case, and case
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     Length 702
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Query Match 38.8%; Score 602; DB 4; I
Best Local Similarity 93.6%; Pred. No. 1.2e-163;
Matches 657; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: DIAMOND, LISA B
APPLICANT: LOGAN, JOHN S
APPLICANT: STRARG, GUERARD W
APPLICANT: STRARM, ALMY
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: RECOMMY AND NEIMARK, P.L.L.C.
STREET: 419 SEVENTH STREET, N.W., SUITE 300
CITY: WASHINGTON
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Best Local Similarity 100.0%; Pred. No. 8e-109;
Matches 412; Conservative 0; Mismatches 0;
CURRENT APPLICATION NUMBER: US/09/612,033B
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 3, Application US/08675773B ; Patent No. 6166288
                                                                                                                                                                                                                                            | NAME/KEY: CDS
| LOCATION: (13)..(411)
| CTHER INFORMATION: tmst2 00004-d1
| US-09-612-0338-5
                                                                                                                                                                                TYPE: DNA ORGANISM: Mus musculus
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Patent No. 6627199
GENERAL INFORMATION:
APPLICANT: Saxis, Chris
TITLE OF INVENTION: tmstz, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: 0 Genes
TITLE OF INVENTION: 0 Genes
FILE REFERENCE: 01017/35434A
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                                                                                                                                                                                                                          PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
OTHER INFORMATION: consisting of Mus musculus sequences and
OTHER INFORMATION: Immunoglobulin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                        Length 1200;
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 514.6; DB 4;
Pred. No. 3.3e-138;
0; Mismatches 19;
  CURRENT APPLICATION NUMBER: US/09/612,033B
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.2%;
Best Local Similarity 96.5%;
Matches 526; Conservative
                                                                                       NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 1200
                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (1)..(1194)
US-09-612-033B-13
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US-09-612-033B-5
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265 AAGGGAGACATTTAATAGGGTCTGGCTTACAGTTTTCAGGAATTTAGTCCATCATGACGGA 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 896 CATCTIGAICTGCAAGGAATAA--AAGGAGACTGTGCCACACTATACACAGCTTGAAC 953
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                                                                                                                                                                                                                                                                                                                                                                                   Length 3791;
                                                                                                                                                                                                                                                                                                                                                                                                                           74; Indels
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APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NATA:
FILING DATE: 27-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                   Score 96.6; DB 3;
Pred. No. 5.5e-17;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1014 CTAATAATACCATTTCTTATGAGGCAAGCAT 1044
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                                                                                                                                     DIAMOND=1A
                 APPLICATION NUMBER: US/08/675,773B
FILING DATE: 03-JUL-1996
CLASSIFICATION: 800
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Patent No. 6090620
GENERAL INFORMATION:
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: DIAM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                    TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3791 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.2%;
Best Local Similarity 69.7%;
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 189; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: GENTITLE OF INVENTION: WEB NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seattle
Washington
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3652 TTCAGAGGTTTAGTCCATTATCA----TGGAAGGCATGGCAGGGTGTACAGGCAGACATG 3705
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Pred. No. 6.5e-14;
0; Mismatches 71; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mulligan, John T.
Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
WERNER'S SYNDROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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ATTORNEY/AGENT INFORMATION:
NAME: MCMasters, David D.
REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 209, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 209:
SEQUENCE CHARACTERISTICS:
LENGTH: 51259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Yu, Chang-En
Oshima, Junko
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COUNTRY: USA
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Best Local Similarity 68.9°
Matches 182, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
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US-08-781-891-209
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FELECOMMUNICATION INFORMATION
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                750 GAGATCCAGACTAAGACAACTCTAAT-AAGGGAAACATTTAATTGGGACTGGCTTACAGT 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      809 TTCGGACGTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATG 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GIGCCACACTATACACAGCTIGAACATAGGAGACCTCAAAGCCTGTCCCCACAGTGACAA 988
                                                                                                                                                                                                                                                                                        5.7%; Score 88.4; DB 4; Length 51259; 68.9%; Pred. No. 6.5e-14; tive 0; Mismatches 71; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: FALKNER, F.
; APPLICANT: SALVERS:
; CORRESPONDENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Follow, & Lardner
; STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
REFERENCE/DOCKET NUMBER: 240052.419C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: SEGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
                                                                                                                                                                                       TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 209: US-09-166-209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          989 ACTICCICCAACAAGGICATACCT 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3822 ACTICCICCAACAAGGCCACACCT 3845
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
                                                                                 INFORMATION FOR SEQ ID NO: 209: SEQUENCE CHARACTERISTICS: LENGTH: 51259 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.9°
Matches 182; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    929
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APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: RTS-0135
CURRENT APPLICATION NUMBER: US/09/657,346A
CURRENT FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 174
                                                                                                                                                                                                                                                                                                                                                               1202 GGTCCACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCAC 1261
                                                                                                                                                                                                                                                                                                                                                                                                                     1262 CTCACTGACTTCCCTTCCCCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAA 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1322 TGTGCCTTCTTGGTTCTTCCTCCTTTCCCCCTCTTCTGGTCCTTACTTCTCTTCTT 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1382 CTCCCACTCTCCACCAGCCTCCTTTAAGGCCTGAATCAGTCTGTAGGTCATGTTTAATC 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                           DB 1; Length 7218;
                                                                                                                                                                                                                                                       Query Match 5.5%; Score 85.2; DB 1; Length 7 Best Local Similarity 3.7%; Pred. No. 1.6e-13; Matches 12; Conservative 216; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1348 YYYYYYYYYYYYYYYYY 1369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1502 CTACAATAAAACCCTTCCCCCT 1523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 96, Application US/09657346A Patent No. 6503754 GENERAL INFORMATION:
TELERAX: (703)000. TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
TOWNTH: 7218 base pairs
                                                            14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (27235)...(27246)
US-09-657-346A-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (19791) ... (19802)
CDS
                                                                                             LENGTH: 7218 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                             , CLONE: pTZgpt-F18
US-08-232-463-14
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                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hong Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (24168) ...
NAME/KEY: CDS
LOCATION: (25696) ...
NAME/KEY: CDS
                                                                                                                                                         TOPOLOGY: line
IMMEDIATE SOURCE:
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US-09-657-346A-96
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NAME/KEY: CDS
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3802 A-CATGGCAGGACCCAGGCAGGCATGGTGC---AGAAGGAGCTGAGAGTTCTACATCTTC 3747
                                                                                                                                    3746 ATCTGAAAGC----TGCTAGCAGAATACTGACTTCCAGGCAGCTAGGACAAGGG---T 3696
                                                                                                                                                                                 963 CTCAAAGCCTGTCCCCACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCTAATAATA 1022
                                                                                                                                                                                                         1020 ATACCATTTCTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTC 1079
                                                                                           903 ATCTGCAAGCAATAAAAGGAGACTGTGTGCCACACTATACACAGGCTTGAACATAGGAGAC 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 AACCTCAAATCCCACCTCCACAGTGACACACTTCTTCCAACAAGGCCA---CCCCTAATA 146
      843 AGCATGGCAGCATCTAAGCAGAACATGATGTTGGAGAAGGAGCTGAGATTTTCTGCATCTTG 902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          900 TIGAICIGCAAGCAATAAAAGGAGACIGIGIGCCACACIATACACAGTIGAACATAGGA 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 TAGATCCACAGGCAGCAAAAGGAGAC--TGTGCCACACTAGGCCTAACTTGAGCTTATAA 89
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08477831C
Patent No. 6429291
GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUWEN, ZHANG
APPLICANT: BYWWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,831C
FILING DATE: 07-JUN-1995
CLASSIFFCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1251 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LECULE TYPE: DNA (genomic)
DESCRIPTION: /desc = "Intron 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY AGENT INFORMATION:
NAME: PIERRI, MARGARET A.
REGISTATION UNDRER: 30,709
REFERENCE/DOCKET NUMBER: SIM-1
TELECOMMUNICATION INFORMATION:
TELEFONE: 212-596-9000
TELEFAX: 212-596-9000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4243 base pairs
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                                                                                                                                                                                                                                                                    1023 CCATTTC 1029
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STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                             US-08-477-831C-7
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Matches 142;
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                                                                                                                                                                                                         22137 AGGTCAGTCCATTAACATCATGGCAGGAAGCATGGCAGGCGTCCAGGTAG-GATGGTGCTG 22195
                                                                                                                                  3862 ACATTTAATTGAAGTTGGCTTACAGGTTCAGTTCAGTACATGATGATCAAGGTGGGA 3803
                                                                                         755 CCAGACTAAGACAACTCTAATAAGGGAAACATTTAATTGGGACTGGCTTACAGTTTCGGA 814
                                                                                                                                                                            815 CGTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGTTG 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     783 ACATTTAATTGGGACTGGCTTACAGTTTTCGGACGTTTTTGTCCATGATTATCATAGTGGGA 842
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA SEQUENCE ENCODING OF THE CPG-1 NEURAL POLYPEPTIDE AND THE POLYPEPTIDE ENCODED THEREBY
                                                 1;
  5.3%; Score 81.4; DB 4; Length 30310; 75.5%; Pred. No. 5e-12; ive 0; Mismatches 36; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.1%; Score 78.6; DB 5; Length 3872; 68.8%; Pred. No. 8.9e-12; tive 0; Mismatches 64; Indels 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12169
PRIOR APPLICATION NUMBER: IL 104097
FILING DATE: 15-DEC-1992
                                                                                                                                                                                                                                                                                          875 GAGAAGGAGCTGAGATTTCTGCATCTTGATC 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20,520
"". CITRI=2 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application PC/TUS9312169
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-JUN-1993
CORRESPONDENCE ADDRESS:
ADDRESSER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Neimark, Sheridan
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: CIT
TELECOMMUNICATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3872 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
Query Match 5.3
Best Local Similarity 75.5
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 15-DEC-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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505..786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , NAME/KEY:
; LOCATION:
PCT-US93-12169-1
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
FILE REPERENCE: 7853-136
CURRENT APPLICATION NUMBER: US/09/245,041
CURRENT FILING DATE: 1999-02-05
EARLIER FILING DATE: 1999-07-21
EARLIER PILING DATE: 1998-10-20
NUMBER: OF SEQ ID NOS: 131
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 90050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5256 CTATAAAGGAAAGCATTTAATTGGGGCTGCCTTACAG-TTCAGAGCTTCAGTCAATTATT 5198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    771 CTAATAAGGGAAACATTTAATTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATT 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            831 ATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGAT 890
147 ATGCCACTCCCTGTGGGCCAAGTA-TCAAACACACACAGTCTCTGAGGGCCATTACTATCA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                         RESULT 14
US-09-917-254-47/c
i Sequence 47, Application US/09917254
j Patent No. 6703204
j GENERAL INFORMATION:
d GENERAL INFORMATION:
i APPLICANT: Baak, Jan
TITLE OF INVENTION: Prognostic Classification of Breast Cancer;
fILE REFERENCE: B0801/7224 (JRV)
CURRENT APPLICATION NUMBER: US/09/917,254
CURRENT FILING DATE: 2001-07-27
PRIOR FILING DATE: 2000-07-28
i NUMBER OF SEQ ID NOS: 102
: SSEPTWARE: Patentin version 3.0
: LENGTH: 5257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 74.2; DB 4; Length 5257;
Pred. No. 2e-10;
0; Mismatches 43; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5137 rrcracarccagarregeagerargarcagegae 5103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  891 TTCTGCATCTTGATCTGCAAGAAAAGGAGAC 925
                                                                     1080 AAACCACCACAGGTTAACAAT 1100
                                                                                                                  206 AACCTCCACCGTATCAAACT 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-245-041-5

Sequence 5, Application US/09245041

Patent No. 6274339

GENERAL INFORMATION:

APPLICANT: MOOZE, K.

APPLICANT: Nagle, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.6%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 76.9
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
CRGANISM: Mus musculus
US-09-245-041-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: Homo Sapiens
US-09-917-254-47
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Sequence Sequence

Sequence 817, App Sequence 247, App Sequence 163, App Sequence 21, App11 Sequence 91, App1 Sequence 91, App Sequence 1687, App Sequence 23, App Sequence 23, App Sequence 23, App Sequence 247, App Sequence 247, App

Sequence 633, App Sequence 139, App Sequence 349, App Sequence 1435, App Sequence 20, Appl Sequence 37, Appl Sequence 37, Appl Sequence 37, Appl

US-10-964-549-737 US-10-1964-549-737 US-10-193-616-5 US-10-087-192-247 US-10-087-192-247 US-10-087-192-247 US-10-942-954-5 US-10-942-954-5 US-10-942-954-5 US-10-942-954-5 US-10-192-1687 US-10-087-192-937 US-10-087-192-937 US-10-087-192-1435 US-10-192-1435 US-10-192-1435 US-10-192-1435 US-10-192-1435 US-10-192-1435 US-10-192-1435 US-10-087-192-1999 US-10-192-1931 US-10-087-192-1999 US-10-087-192-1999 US-10-087-192-1999 US-10-087-192-1999 US-10-087-192-1999 US-10-087-192-1999 US-10-192-1999 US-10-192-1129

Sequence 1999, Ap Sequence 1891, Ap Sequence 905, App Sequence 63, Appl Sequence 767, Appl

Sequence

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DB 17; Length 1550;

Score 1550; Pred. No. 0;

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Sequence of Application US/10622407

Sequence of Application US/10622407

Publication No. US20040018544A1

GENERAL INFORMATION:
GENERAL INFORMATION:
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GENERAL INFORMATION:
TITLE OF INVENTION: MENBER OF THE THE RECEPTOR SUPERFAMILY OF GENES
FILE REPERENCE: 01017/35434B

CURRENT APPLICATION NUMBER: US/10/622,407

CURRENT APPLICATION NUMBER: US 09/612,033

PRIOR APPLICATION NUMBER: US 09/612,033

PRIOR APPLICATION NUMBER: US 60/143,063

PRIOR PILING DATE: 2000-07-07

PRIOR FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (13)..(606)
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Publication No. US20030096355A1

GENERAL INFORMATION:

APPLICANT: Zhang, Ke

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE REFERENCE: 01017/35551A

CURRENT APPLICATION UNMER: US/10/193,616

FILE REFERENCE: 01017/35551A

CURRENT FILING DATE: 2002-07-11

PRIOR APPLICATION NUMBER: US/09/611,989

PRIOR APPLICATION NUMBER: US 60/143,137

PRIOR APPLICATION NUMBER: US 60/143,137

PRIOR APPLICATION NUMBER: US 60/143,137

PRIOR FILING DATE: 1999-07-07

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 15

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ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(531)
OTHER INFORMATION: Mu-ymkz5
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TMST2, A NOVEL
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; Sequence 13, Application No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANTO. Chris
; APPLICANT: Saris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2;
; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US 105/10/622,407
; PRIOR FILING DATE: 2003-07-17
; PRIOR FILING DATE: 1999-07-09
; PRIOR FILING DATE: 1999-07-09
; SEQ ID NOS: 15
; SEQ ID NO 13
; LENGTH: 1200
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                   AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
                                                                           GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCC
                                                                                               CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.2%; Score 514.6; DB 17; Length 1200;
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; LOCATION: (1)..(1194)
US-10-622-407-13
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TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TWST2, A NOVEL
TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
FILE REPERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2003-07-17
PRIOR PPLICATION NUMBER: US 09/612,033
PRIOR PELING DATE: 2000-07-07
PRIOR PPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 9
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     GAGTGTGCTAATTGTGTCCGTTGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/10622407; Publication No. US20040018544A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Primer 2086-39 US-10-622-407-9
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LOCATION: (13)..(552)
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US-10-622-407-9
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APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sande, Arthur T.
TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
FILE REFERENCE: LEX-0102-USA
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT PILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR APPLICATION NUMBER: US 60/168,358
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FRRESCO for Windows Version 4.0
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                                  Indels
              Pred. No. 2.1e-103; 
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 737, Application US/09728445; Patent No. US20020102543A1; GENERAL INFORMATION:
100.0%; Pre-
                                    Conservative
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ORGANISM: Mus musculus
US-09-728-445-737
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Best Local Similarity
Matches 403; Conserv
                Best Local Similarity
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                                      412;
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Sequence 5, Application US/10622407

Publication No. US20040018544A1

GENERAL INFORMATION

TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

TITLE OF ILING DATE: 2003-07-17

CURRENT APPLICATION NUMBER: US/10/622,407

CURRENT APPLICATION NUMBER: US 60/143,063

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SED ID NO 5

LENGTH: 412
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                Pred. No. 1.3e-131;
0; Mismatches 19; Indels
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US-10-622-407-5
            96.58;
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                                  526; Conservative
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LOCATION: (13)..(411)
            Best Local Similarity
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190 CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 249
                                                                                                         TTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCCAAGGAATCCCTGTCCTCCAGGAA 480
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals
FILE REFERENCE: LEX-028-USA
CURRENT FILING DATE: 2004-10-13
FRICH APPLICATION NUMBER: US/09/750,456
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 403; Conservative
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ORGANISM: Mus musculus
US-10-964-549-737
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US-10-964-549-737
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                                                                                            and Characterization of
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; Sequence 817, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Mortis, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR;
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 253.2; DB 14;
Pred. No. 2.1e-59;
0; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 87.9%;
Matches 276; Conservative
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; LOCATION: (6)..(356)
US-10-193-616-5
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                                                                                                                                                                                                      Length 124289;
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Pred. No. 8.9e-45;
0; Mismatches 84; Indels
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APPLICANT: MOSTIS.

APPLICANT: Engelhard, Eric K.

TITLE OF INVENTION: NOVER COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122

CURRENT APPLICATION NUMBER: US 09/747,377

PRIOR PILING DATE: 2000-03-01

PRIOR PILING DATE: 2000-03-02

NUMBER OF SEQ ID NOS: 2059

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH. 203070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1055 GAGTCTATGAGGGCCAAACCAATTCAAACCACCACAGGTT 1094
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 247, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1) ... (203070)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-247
                                                                                                                                    , LOCATION: (1)...(124289)
; OTHER INFORMATION: n = A,T,C or US-10-087-192-817
                                                                                                                                                                                                13.3%;
Best Local Similarity 75.3%;
Matches 256; Conservative
                                                                                 ORGANISM: Mus musculus
                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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                                                  LENGTH: 124289
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US-10-087-192-247
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                                                                                                      FEATURE:
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Gaps

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193625 ACTATAAGCCACACTGGGCATAACTTGAGCACATGAGACATTAAAGCCTGCCCCAACAGT 193684
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                                                           97339 ATGGTGGGGGGGGAGAAGCTGAGAGTTCTACATCTGGATCCACAGACAAGCAGCCAAAAAG 97398
                                                                                                                                                                                                                                                                                                                                                                                                   97459 cacactriccriccaacaaagccacacciccraaragreccactriccrargagccaagcarr 97518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCATTTCTTATGAGGCAAGCATT 1045
                                                                                                                       865
747 ACAGAGATCCAGACTAAAGACAACTCTAAT-AAGGGAAACATTTAATTGGGACTGGCTTAC 805
                                                                                                                                                                                                                                            747 ACAGAGATCCAGACTAAGACAACTC-TAATAAGGGAAACATTTAATTGGGACTGGCTTAC 805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           806 AGTTTCGGACGTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               806 AGTTTCGGACGTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGAC
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                                                                                                                                                                                                                                                                                                                                                                   926 TGTGTGCCACACTATACACAGGCTTGAACATAGGAGACCTCAAAGCCTGTCCCCACAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 187.6; DB 21; Length 721377; ilarity 77.8%; Pred. No. 2.3e-39; Conservative 0; Mismatches 69; Indels 3; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1046 CAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCACCACAGGTTA 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REFERENCE: 529452001800
CURRENT APPLICATION NUMBER: US/10/461,862
CURRENT FILING DATE: 2003-06-13
NUMBER OF SEQ ID NOS: 184
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 163
LENGTH: 721377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1044 TTCAAACACATGAGTCTATGAGGG 1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 163, Application US/10461862; Publication No. US20050090434A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(721377)
OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(721377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 252; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-461-862-163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57061 GCCCAACTCCACAATGACACACTTCCTCCAACAAGGCCACACGCTTAATAGTAGTACCACTT 57120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCTGTCCCCACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCTAATAATAACATTT 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      849 GCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGATTTCTGCATCTTGATCTGC 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                909 AAGCAATAAAAGGAGACTGTGTGCCACACTATACACACTTGAACATAGGAGACCTCAAA 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             789 AATTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATTATCATAGTGGGAAGCATG
                                                                                                                                                                                                                                                                                                                                                                                                               Score 187; DB 19; Length 111836;
Pred. No. 1.2e-39;
0; Mismatches 60; Indels 0;
                                                                                     Sequence 51, Application US/1032281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: David W. Morris
TITLE OF INVENTION: Novel Compositions and Methods in Cancer FILE REFERENCE: 529452001000
CURRENT APPLICANTS: 2002-12-17
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PAGESEQ for Windows Version 4.0
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57121 ccrigriegeccaagcarrcaaacacaegagrrreregageccaa 57163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTTATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193745 TTCAAACATATGAGTCTAAGGGGG 193768
                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature; LOCATION: (1)...(111836); CTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-942-954-2; Sequence 2, Application US/10942954; Publication No. US20050144662A1
                                                                                                                                                                                                                                                                                                                                                                                                              12.1%;
78.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 223; Conservative
                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                           LENGTH: 111836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696
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2826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              930 TGCCACACTATACACAGCTTGAACATAGGAGACCTCAAAGCCTGTCCCCACAGTGACAAA 989
                                                                                                                                                                                                                            750 GAGATCCAGACTAAGACAACTCTAATAAGGGAAAACATTTAATTGGGACTGGCTTACAGTT
                                                                                                                                                                                                                                                                    2767 GACACCATGACCTGGGTAATTTTCATAAAGAAACATTTAATTGGTACTGGCTTACAGTT
                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                Indels
                                                                                                                                  Score 186; DB 22;
Pred. No. 8e-40;
0; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1048 AACACATGAGTCTATGAGGGCCAAACCAATTCAA 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3065 AACACTIGAGICTATGGGGTCATTICTCTTTTAA 3098
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Job time : 3525.54 secs
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                                                                          ģ
                                                                          ΰ
                                                                                                                                    Query Match
Best Local Similarity 76.3%;
Matches 255; Conservative
FEATURE:

NAME/KEY: misc_feature

LOCATION: (6)..(6)

OTHER INFORMATION: n is a,
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us-10-622-407-7.rst

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

September 8, 2005, 13:43:46; Search time 18110.6 Seconds (without alignments) 3257.733 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

34239544 seqs, 19032134700 residues Searched:

68479088 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

EST: * Database

99 est1: 90 est2: 90 est2: 90 est3: 90 est4: 90 est6: 90 est6: 90 est6: 90 est6:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Query				
No.	core	Matc	ength	\overline{a}	۵	
-	1521.8	98.2	4224	3	BC076592	BCO
7	1475.8	95.2	2276	m	AK012838	AKO:
е	761.4	49.1	1003	9	BY711952	BY71
4	752.4		756	۲	CK634366	CK6:
S	751.4	48.5	765	7	CN461442	CN4
Q	734.2	47.4	784	9	CB723050	CB7;
		1		•		

Description	BC076592 Mus muscu	AK012838 Mus muscu	BY711952 BY711952	CK634366 UI-M-HNO-	CN461442 UI-M-HB0-	_	CB525851 UI-M-FY0-	BU611594 UI-M-FIO-	CF729486 UI-M-HD0-		CB587413 AGENCOURT	BI788944 ie41e08.y		BG077775 H3019F06-	BQ033912 UI-1-CF0-	AW538894 C0113B08-		BQ031584 UI-1-CF0-	•	CG651536 OST412784	CG535649 OST122794	CN697902 E0401A05-	CK333918 H8266D02-	BB613091 BB613091	
Ω	BC076592	AK012838	BY711952	CK634366	CN461442	CB723050	CB525851	BU611594	CF729486	AW544660	CB587413	BI788944	CN687949	BG077775	BQ033912	AW538894	AA182278	BQ031584	AA754807	CG651536	CG535649	CN697902	CK333918	BB613091	
8	m	m	9	7	7	9	9	5	7	~	9	4	7	4	ហ	~	~	'n		σ	σ	7	7	7	
% Query Match Length DB	4224	2276	1003	756	765	784	708	969	683	552	863	480	614	639	458	447	438	437	411	410	415	597	489	585	
% Query Match	98.2	95.2	49.1	48.5	48.5	47.4	45.7	44.8	43.3	34.8	32.6	29.7	29.3	28.9	28.3	28.0	27.6	26.9	26.3	26.1	25.3	24.5	23.8	23.5	
Score	1521.8	1475.8	761.4	752.4	751.4	734.2	708	694.4	670.4	539.2	505.4	460.4	454.8	448.2	438.8	434.2	428.4	416.2	407.8	404	392	380	369.6	364	
Bult No.	٦	8	٣	4	2	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	

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487 6 CA879824 487 6 CA879822 430 4 BE0918267 430 8 AQ978007 469 8 AQ978007 331 5 BY182663 331 5 BY3482663 331 5 BY348266 438 7 CN692087 438 7 CN692087 438 7 CN692087 438 7 CN692087 430 7 CN692087 431 5 BY183172 431 5 BY185969 341 5 BY18583696 5297 2 BR381534 755 8 AZ583966	BY527094 BY527094 CA879822 K0978B09- BG918267 K02818449		B1343934 B1343934 BY208766 BY208766 BY345556 CN692087 B0318B06-		BB873121 BB873121 BY036522 BX036522 AI747041 ull2g01.y BY325940 BX325940	BE381534 601272537 AZ836976 2M0132M06 AZ583966 1M0388L12
8 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	BY527094 CA879822 BC919267	BB784219 AQ978007 BY182663	BY343934 BY208766 BY345556 CN692087	CF578223 BY183172 BY195969 BY010018	BB873121 BY036522 AI747041 BY325940	BE381534 AZ836976 AZ583966
	0 7 c	1007	147.8 18.67	8040 7000	7 T 4 8	9 8 7
	23.4	222.1	19.6	18.4 18.0 17.2	15.0 14.8 14.7 14.4	14.3 14.2 14.0
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	5 5 7 7 7 7	30 5 30 5 30 7 30 7	33 3 3 3 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	35 36 37 38	8 4 4 4 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	44 44 5

ALIGNMENTS

RESULT 1

BC076592	
LOCUS	
DEFINITION	Mus musculus tumor necrosis factor receptor superfamily, member 22,
	mRNA (cDNA clone IMAGE:30652769).
ACCESSION	
VERSION	BC076592.1 GI:50370338
KEYWORDS	HTC.
SOURCE	Mus musculus (house mouse)
ORGANISM	
	Chordata;
	Rodentia;
REFERENCE	1 (bases 1 to 4224)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
	Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
	Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
	Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., H81eh, F.,
	Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
	Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
	Scheetz, T.E., Brownstein, M.J., UBdin, T.B., ToBniyuki, S.,
	Carningi, P., Frange, C., Mana, S.S., Loqueiiano, N., Peters, G.J.,
	Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,
	MCKernan, K.J., Malek, J.A., Cunarache, P.H., Kichara, S.,
	Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
	VILIAION, D.K., MUZNY, D.M., SOGEIGIEN, E.D., LU, A., GIDDS, R.A.,
	Fanely J., Helicol, S., Nettennah, M., Madan, A., Noully S., S.,
	Sanchez, A., Whiting, M., Madah, A., Young, A.C., Shevchenko, I.,
	Bouliaid, G.G., Blakesley, R.M., Ioucimman, O.W., Green, B.D.,
	Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, K.M.,
	Butterfield, Y.S., Krzywinski, M.I., Skaiska, U., Smailus, D.E.,
	Schnerch, A., Schein, J.B., Jones, S.J. and Marra, M.A.
97111	Celleration and intriar analysis of more than 13,000 turn-resident
TAMBIAT	numan and mouse culm, sequences Proc Mrtl Ard Gri II C A GG (26) 16809-16901
GENERAL	FIGURE ANGLE ACTE C.C.A. (201, 1007) -1000 (1004)
PEFERENCE	2 (bases 1 to 4224)
AITTHORS	
TITLE	Direct Submission
JOURNAL	Submitted (06-JUL-2004) National Institutes of Health, Mammalian
	Gene Collection (MGC), Cancer Genomics Office, National Cancer
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
2000	USA VICTORIAN TITLE BELLEVILLE AND
COMMENT	Contact: MGC help desk
	Email: cgapb-r@mail.nih.gov
	Tissue Procurement: Dr. Jim Lin, University of Iowa
	cDNA Library Preparation: M. Bento Soares, University of Iowa
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A COLUMN TOWN

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TGGTCCACTGTGGTTCCTATTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCA 1260
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AK012838 AK012838 I GI:12849843 HTC; CAP trapper.
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This clone has the following problem: clone inconsistent with known
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu.I., Bair.T., Bair.J., Grouch.K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
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Pred. No. 0;
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/tissue type="Eye"
/clone_Tib="NIH BMAP_HB0"
/lab_host="DH10B"
/note="Vector: pYX-ASC"
                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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/note="unnamed protein product;
receptor superfamily member 21
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/strain="C57Bl/6J"
/db_xref="FANTOM_DB:2810028K06"
/db_xref="taxon:10090"
/clone="2810028K06"
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Pred. No. 0;
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/db_xref="G1:26377809"
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

E (bases 1 to 2276)

& dachi, J. Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramcto, K., Furuno, M., Hanagaki, T., Maca, H., Kojini, Y., Ichi, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojini, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matcuyama, T., Myazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Sakai, C., Sakai, K., Sano, H., Saato, R., Sakai, C., Sakai, K., Sano, H., Saakai, K., Sahinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Yoshida, K., Shibata, Y., Yoshida, K., Yoshida, K., Yoshida, K., Yoshida, K., Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GARAGAGAAGAGACTCTTTTTTTTTTTTYN 3'], cDNA was prepared by using trebalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went
                                                                                                                                                                                                                                                               Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumco,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Mus musculus (house mouse)
Mus musculus
Eukarnota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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High-efficiency full-length cDNA cloning
wheth. Enzymol. 303, 19-44 (1999)
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musculus cDNA clone 2810028K06 5', mRNA sequence

Mus musculus (house mouse) BY711952 BY711952.1 GI:27123215

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Mus musculus

ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

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Lutert Submission.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pkulda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
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Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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BY711952 1003 bp mRNA linear EST 16-DEC-2002 BY711952 RIKEN full-length enriched, 10, 11 days embryo whole body

BY711952 LOCUS DEFINITION RESULT 3

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Pred. No. 3.5e-177;
0; Mismatches 6;
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/db xref="taxon:10090"
/clone="2810028K06"
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/cloue 1103" Whe brake Annual brake Containing a Not I site. Double strand cDNA was primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with NotI and then cloned directionally into pXT-Aso vector. The library tag sequence located between the Not I site and the polyA tail is CGAACTGAAT. This library was created for the University lows Brain Anatomy Project (BMAPP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                        CK634366 756 bp mRNA linear EST 28-JAN-2004
UI-M-HNO-cnj-e-07-0-UI.rl NIH_BMAP_HNO Mus musculus cDNA clone
IMAGE330640134 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Email: cgapbs.r@mail.nih.gov
Contact: Robert Strausberg, Ph.D.
Email: cgaps.r.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Clone Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefl.html
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Sciurognathi, Muridae, Murinae, Mus
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The following repetitive elements were found in this cDNA sequence: 119-146, > (TAAAA)n#Simple_repeat (matched compliment) 151-201, > 91_MM#SINE/Alu (matched compliment) 194-535, >ORRIB#LTR/Malk (matched compliment)
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/db_xref="taxon:1090"
/dlone="twAGE:30640134"
/tissue_type="Upper Head"
/dev_tage="9.5"10.5 dpc"
/lab_host="DH108"
/clone_lib="NIH_BMAP_HN0"
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larity 99:6%; Pred. No. 5.6e-175;
Conservative 0; Mismatches 3;
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Mammalia; Butheria; Rodentia;
1 (bases 1 to 756)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Mus.
S NIH-MGC http://mgc.nci.nih.gov/.
Interpolation Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl.html
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/tissue types="whole eye"
/dev stage="whole eye"
/dev stage="whole eye"
/dev stage="whole (TI phage resistant)"
/lab_host="Null BMAP HBO"
/clone lib="Null BMAP HBO"
/note="Organ: Eye; Vector: pXx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Sonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.Pirst strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction ,ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
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This clone was contributed by the Brain Molecular Anatomy Project
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                      (BMAP)
The following repetitive elements were found in this CDNA sequence: 75-111, > (CAG)n#Simple_repeat (matched compliment) 683-710, > (TAAAAA)n#Simple_repeat (matched compliment) 715-765, > 1 MA#SINE/Alu (matched compliment) 715-765, Seq_primer: pXX-5.
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ilarity 99.5%; Pred. No. 9.9e-175;
Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:30652769"
                                                                                                                                                                                                                location/Qualifiers
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UI-M-FYO-cfe-p-15-0-UI.rl NIH_BMAP_FYO Mus musculus cDNA clone
IMAGE:6848608 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 cresreaaracresreraaasasseresresrasaacresresresrescassares 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTC 360
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Developing Mouse Nervous System', supported by Institute of Mental Health (NIMH), Hemin Chin, program coordinator."
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                                                                                                                                           Length 784;
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                                                                                                                                           47.4%; Score 734.2; DB 6; 99.0%; Pred. No. 1.8e-170; iive 0; Mismatches 3;
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// gtrain="C57BL/6"
// db xref="raxon:10090"
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// clone="TMAGE:684100"
// dev stage="I, 5, and 15 days newborn"
// dev stage="I, 5, and 15 days Genstrated according
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// dev stage="I, 5, and 15 days days newborn"
// dev stage="I, 5, and 16 dested with Not I and then cloned
// directionally into pXx-Asc vector. The library tag
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Email: cgapbs-r@mail.nih.gov.

Email: cgapbs-r@mail.nih.gov.

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

The following repetitive elements were found in this cDNA

sequence: 26-62, >(CAG) m#Simple_repeat (matched compliment)

634-661, >(TAAAA) n#Simple_repeat (matched compliment)

649-661, >(TAAAA) m#simple_repeat (matched compliment)

Seq primer: pXx-5.
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UI-M-GH0-cel-e-02-0-UI.rl NIH BMAP_GH0 Mus musculus cDNA clone
IMAGE:6841035 5', mRNA sequence.
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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580 540 640 909 700 9 760 820

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base 1 to 696)

1 (base 1 to 696)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 Unpublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa CDNA Library Library arrayed alstribution: Clone distribution information can be obtained from Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento soares@ulowa.edu
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UI-M-FIO-cav-h-06-0-UI.rl NIH BMAP FIO Mus musculus cDNA clone
UI-M-FIO-cav-h-06-0-UI 5', mRNA sequence.
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/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
/lab_bost="HIOB (TI phage resistant)"
/clone_lib="NXH BNAP FI0"
/note="Organ: Brain; Vector: pXX- Asc; Site_1: EcoR I;
                                                                                                                           301 ATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAGTGCC
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/mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                                                                                                                                                                  Email: cgapbs-remail.nib.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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708; Conservative 0; Mismatches 0;
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/strain="C57BL/6"
                                    Mus musculus (house mouse)
Mus musculus
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유 ò 요 à 셤 ò 셤 IMAGE:30614762 5', mRNA sequence

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Site 2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with ECOR I adaptor, digested with NotI and then cloned directionally into PXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CACCACCAC. This library was created for the University low Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
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44.8%; Score 694.4; DB 5; Length 696;
Best Local Similarity 99.9%; Pred. No. 1.2e-160;
Matches 695; Conservative 0; Mismatches 1; Indels 0.
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CF729486 683 bp mRNA linear EST 09-OCT-2003 UI-M-HD0-cld-d-03-0-UI.rl NIH_BMAP_HD0 Mus musculus cDNA clone

CF729486 LOCUS DEFINITION

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/tissue type="whole eye"
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Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soarces, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1# agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231
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Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                 NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:10090"
/clone="IMAGE:30614762"
                                                                                                                         Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                     Mus musculus (house mouse)
Mus musculus
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CF729486.1 GI:37603654
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Walrches 682; Conservative
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KEYWORDS
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                                                     GCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTAT 411
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                                                                                                                                                                         GACCCAAAATTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTC 419
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 muouse developmental CDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
GATAATTACCTGGATGCTTGTATACTTTGCTCCACCTGTGAT-AAGATCAGGAAATGGTG
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                                                                                                                                                                                                                 CTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAATCCCAGA
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/db_xref="niaEST:C0184C12-3"
/db_xref="taxon:10090"
/clone="C0184C12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       712 GAACTTGATTTGAAGACCAGGCTG 735
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SOURCE

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Site 1: SalI; Site 2: NoII; Total RNAs were extracted from 5 EPG. The double-Stranded cDNA was synthesized by Gibco's kit with an Oligo(dT) primer [NoII primer-adapter
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clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         552 CACAGTGACAAACTTCCTCCCAACAAGGTCATACCTCCTAATAATAACACATTTCTTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252 CCCCTAGCTTCTCATTCCCAGGTAACCCTGCCATTTTTTGGTAATGTGCCTTCTTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192 TICCTCTTTCCCCCTCTCTTCGGTCCTTATTTCTCTTCCTCTCCCACTCTCCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCTAATAATACCATTTCTTATGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1038 CAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCACCACAGGTTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1338 TICCICICICITICCCCCTCTCTTCTGGICCTTACTICTTCCTCCCACTCTCCACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1218 TATTAACATACTGAAGAACATGACCTCACCTTACACGTCTCCACCTCACTGACTTCCCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 CTCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCTCTCTTTTTTAAAAACCCTT
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                               /note="Vector: pSPORT1 (Gibco/BRL Life Technology);
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 552;
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Pred. No. 3.1e-122;
0; Mismatches 8;
                                                                                                       from GibcoBRL
                                                                                                                                                                                                                                                                                                                                                                                                                                              34.8%;
98.6%;
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                                                                                                                                                                                                                                                                                                                     1. .480
/organism="Mus musculus"
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/lab host="DH108 (phage-resistant)"
/cloon lib="WHH MGC 136"
/note="Wector: pGWV-SPORT6"
/note="Wector: pgw-million"
/
      EST 03-APR-2003
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                                                                                                                                                                                                                 Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 863)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                        Mathonia institutes of nearth, mammaires concerned in Mathonia should shed (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. David Rowe

CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Plate: NDAM342 row: a column: 02
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CBS87413
AGENCOURT_12970406 NIH_MGC_136 Mus musculus cDNA clone
IMAGE:30294625 5', mRNA sequence.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:30294625"
                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                             CB587413.1 GI:29505269
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Matches 512; Conservative
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/dloo= llb="kxestner ngn3 wt"
/note="Organ: pancress; Vector: pSPORT1 (GIBCO); Site_1:
/note="Organ: psncress; Vector: psncress; V
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                                                                                                                                                                                        361 CTCTCCACCAGCCGCCTCTTAAGGCCTGAGTCAGTCTGCAGGCCATGTTTAATCTACTAC 420
                                                                                                                                                                                                                                                                   TITCICICICICCTGGACTCATCCAGATGTCTCTGGCTGAGCTCTCCCCTCCTACTACTACAA 480
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Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Pax: 617-495-857

Fax: 617-495-857

Fax: 617-495-857

Pancias was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Scearce (mscearce@mail.med.upenn.edu)

Seq primer: -40RP from Gibco
High quality sequence stop: 429.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 480)
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Unpublished (2000)
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E (Bases 1 to 614)
Sharov, A.A., Piao, Y., Matoba, R., Dudekula, D.B., Qian, Y.,
VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C.,
Wang, Y., Carter, M.G., Hamatani, T., Alba, K., Akutusu, H., Sharova, L.,
Tanaka, T. S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S.,
Nagaraja, R., Boheler, K.R., Taub, D., Hodes, R.J., Longo, D.L.,
Schlessinger, D., Keller, J., Klotz, E., Kelsoe, G., Umezawa, A.,
Vescovi, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A.,
D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.
Transcriptome analysis of mouse stem cells and early embryos
Contact: Dawood B. Dudekula
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       614 bp mRNA linear EST 17-MAY-2004 E0250A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:E0250A07 IMAGE:30854118 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATTICITATGAGGCAAGCATTCAAACACAGGGTCTATGAGGGCCAAACCAATTCAAAC 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAAAGCCTGTCCCCACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCTAATAATAC 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAAGCCTGTCCCCACAGTGACAAACTTCCTCCAACAAGGTCATACCTCCCTAATAATAC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATTICITATGAGGCAAGCATTCAAACACATGAGTCTATGAGGGCCAAACCAAATTCAAAC 438
                                                                                                                                                                                                    CATTTAATTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATTATCATAGTGGGAA 198
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                                                                                                                          AAGACCAGGCTGGCCTCAAAATCACAGAGATCCAGACTAAGACAACTCTAATAAGGGAAA 138
                                                                                                                                                                                                                                                                                                                            GCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGCAGCTGAGATTTCTGCATCTTGA 258
GCATGGCAGCATCTAAGCAGACATGATGTTGGAGAGAGGAGCTGAGATTTCTGCATCTTGA
                                                                                                                                                                                                                                                                                                                                                                                 TCTGCAAGCAATAAAAGGAGACTGTGTGCCACACTATACACAGCTTGAACATAGGAGACC
                                                                                                                                                                          CATTITAATTIGGGACTGGCTTACAGTTTTCGGACGTTTTTGTCCATGATTATCATAGTGGGAA
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Plate: E0250 row: A column: 07
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|mol_type="mRNA"
|strain="129Svfrac"
|db_xref="niaeST:E0250A07-5"
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/clone="NIA:E0250A07 IMAGE:30854118"
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29.3%; Score 454.8; DB 7; Length 614; llarity 85.5%; Pred. No. 2.4e-101; Conservative 0; Mismatches 57; Indels 37 Query Match Best Local Similarity Matches 556; Conserv

Gaps

Indels 37;

166 9 TGCCCTTGCAGGTAAAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTG 1 TGTTCTTGCCGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGATGGTG

346 240 180 181 GGAAAGATAATGGCCTGCATGATTGTGAACTTTGCTCCACCTGTGATAAAGACCAGAATA 287 AGAAAGATAATTACCTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAA 121 g à

360 406 300 466 301 ACTATGACCAAAATTTCCGGAATCATGCCGCCCATGTACCAAGTGTCCCCAAGGAATCC recreacreacrerecececedareacesaaareceasereceaaradererer TGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCCAGTGCCGAACAGGTCTTTACT ACTATGACCCAAAATTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCC 347 241 407 g ò

586 453 CCAGAAACCGGCTGTTCCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTCCGTTGTTG ----GCTAATTG CCAGAAACTGGCTGTTCCTACTGAT-----527 421 ઠે 셤

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Other ESTs: H3019F06-3
Cother George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdn@@lgan.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3019 row: F column: 06
Seq primer: -21M13 Reverse
High quality sequence stop: 639
POLYA=NO.
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/clone lib="NIA Mouse 15K CDNA Clone Set"
/clone lib="NIA Mouse 15K CDNA Clone Set"
/note="Vector: pSPORTI; Site=1: Sal1; Site=2: NotI; This clone is among a rearrayed set of 15,247 clones from liberation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased
                                                                                                                                                                                                                                                                             EST 17-DEC-2003
 645
                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (Dases 1 to 639)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X., Garbovac,M.J., Pantano,S., Sano,Y., Placo,Y., Nagaraja,R., Doi,H., Wood,W.H. III. Becker,K.G. and Ko.M.S. H. Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
                                                                                                                                                                                                                                                  639 bp mRNA linear EST 17-DEC-:
H3019P06-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
H3019P06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="H3019F06"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
TGTCTTGAACTTGATTTGAAGACCAGGCTGGACTCAAAATCACAGAGATC 755
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/db_xref="taxon:10090"
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/mol_type="mRNA"
/strain="C57BL/6J"
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458 bp mRNA linear EST 27-MAR-2002 UI-1-CF0-amg-a-07-0-UI.81 NCI CGAP PITT1 Mus musculus CDNA clone UU-1-CF0-amg-a-07-0-UI 3', mRNA sequence. B0033912.1 GI:19769184 EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGGTAACAC 450
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                 31 GITCCTCTTGCTGCTGCTGCTGAATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATC 90
                                                                                                                   8
gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 GAAGTGTCACCCAGGAACATTCACAGGGAAAAGATAATGGCCTGCATGATTGTGAACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              501 TGTGTGCAGTTCATCTGTTTCAAATCCCAGAAACCGGCTGTTCCTACTGTTATCACCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGGTAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561 GAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGAAAAGGTTCTACAG
                                                                                                                                                                                                                                                                             37; Gaps
                                                                                                                                                                                                                     Length 639;
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                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                  Score 448.2; DB 4;
Pred. No. 1.1e-99;
0; Mismatches 58;
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Mus musculus
                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.3%;
Matches 550; Conservative
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/clone="UI-1-CF0-amq-a-07-0-UI"
/tissue_type="Trophoblast"
/lab host="DH10B (Life Technologies)"
/clone=lib="NCI CGAP PITI1"
/clone=lib="NCI CGAP PITI1"
/note="Organ: Placente; yetcor: pT713-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP PITI1 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I; and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)3 tail. The sequence tags for this library are GTGTG, ATCAT, GGGTG, GGTTG. For additional information, contact: Bento Soares,
                                                                                                                                CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@dulowa.edu

The following repetitive elements were found in this CDNA sequence: 18-305, >RMERIOA#LTR (matched compliment)

POLYA-Yes.
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                       Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Minoru Ko, Dr. Janet Rossent, Dr. Janet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.3%; Score 438.8; DB 5; Length 6
Best Local Similarity 97.4%; Pred. No. 2.1e-97;
Matches 446; Conservative 0; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="C57BL/6J"
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  Unpublished (1997)
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Search completed: September 9, 2005, 06:50:08 Job time : 18117.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

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Run

2 ; Search time 598.714 Seconds (without alignments) 127.905 Million cell updates/sec

1087 1 MFGFFCSLVSSLSRWFLMRR.....LLSPLSVLIVSVVVFRIIRR 198 US-10-622-407-8 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

2105692 segs, 386760381 residues Searched:

Total number of hits satisfying chosen parameters:

2105692

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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uo	Mouse tms	Murine tm	Amino aci	Mouse ymk	Mouse 7F4	Mouse ymk	Mouse	Novel	Mouse ymk	Murine TA	Mouse TNF	TNFR1 exp	Murine tu	Моцве Fas	Murine Fa	Murine Fa	пРав веди		Amino aci						
Description	Abw02715	Adj45752	Abw02717	Adj45758	Abw02716	Adj45754	Abw02714	Adj45750	Aaw80254	Adf57551	Adm46623	Adf57557	Adm46624	Abg09344	Adf57549	Abb81467	Adf57553	Aa022289	Adt08167	Adf57552	Aar41688	Aar78611	Aar92530	Aaw86241	Aab19344
0	ABW02715	ADJ45752	ABW02717	ADJ45758	ABW02716	ADJ45754	ABW02714	ADJ45750	AAW80254	ADF57551	ADM46623	ADF57557	ADM46624	ABG09344	ADF57549	ABB81467	ADF57553	AA022289	ADT08167	ADF57552	AAR41688	AAR78611	4AR92530	AAW86241	AAB19344
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% Query Match	100.0	100.0	88.5	88.5	87.9	87.9	68.8	68.8	68.7	68.7	68.7	65.4	62.8	49.9	43.0	29.4	20.8	20.8	20.8	20.1	20.1	20.1	20.1	20.1	20.1
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ALIGNMENTS

ABW02715 standard; protein; 198 AA. ABW02715

ABW02715;

(first entry) 11-MAR-2004 Mouse tmst2-receptor protein.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory; disease; chromosome mapphing; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse.

Mus musculus

US6627199-B1.

30-SEP-2003.

07-JUL-2000; 2000US-00612033

99US-0143063P. 09-JUL-1999;

(AMGE-) AMGEN INC.

Saris C;

WPI; 2003-874309/81. N-PSDB; AAD64754 New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping

Claim 1; SEQ ID NO 8; Opp; English.

The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome

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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diseaminated intravascular coagulation; haemorrhagic shock; hepstitis; insulin resistance; leprosy; leukaemia; lymphoma; meniapitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLL 180
                                                                                                                                                                                                                                                                                                  MFGFFCSLVSSLSRWFLWRRLILLILLILLILLILLILLVVKFAMLELHSFKCPAGEYWSKDVCC 60
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gene therapy. The
in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.
                                                                                                                                                                                                                                                                  1 MFGFFCSLVSSLSRWFLWRRILLILLILLILLINLPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                          Length 198;
                                                                                                                                                                                                               Indels
  identification or mapping. The invention is useful in present sequence is mouse tmst2-receptor protein used exemplification of the invention
                                                                                                                                          Score 1087; DB 7; Pred. No. 1e-81;
                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; SEQ ID NO 8; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJ45752 standard; protein; 198
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                                                                                                                                                                                     Best Local Similarity 100.
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine tmst2-receptor.
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N-PSDB; ADJ45751
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                                                                                                             Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-1999;
07-JUL-2000;
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                                                                                                                                                             Query Match
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ADJ45752
ADJ4572
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syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetees mellitus, disseminated intravascular coagularion, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organia, rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ADDS), tuberculosis and a number of viral diseases. This sequence represents the murine tmst2-receptor polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                              61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
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                                                                                                                                                                                                                                                                                                       KNCSAGTFVKAPCEI PHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS
                                                                                                                                                                                                                                                                                                                                                                                                                                       DRKCOCRTGLYYYDPKFPESCRPCTKCPQG1PVLQECNSTANTVCSSSVSNPRNRLFLLL
                                                                                                                                                                                                                                                                                    1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.
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                                                                                                                                                                                                       100.0%; Score 1087; DB 8; Length 198; 100.0%; Pred. No. 1e-81; cive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPLSVLIVSVVVFRIIRR 198
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                                                                                                                                                                                                                                                 Conservative
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Chimeric - Homo sapiens.
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nes 198; Conserv
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                                                                                                                                                                        Sequence 198 AA;
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                                                                                                                                     invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121
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                                                                                                                                                                                                           Query Match
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The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TMF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is a fusion protein comprising mouse tmst2- receptor protein and human immunoglobulin Fc region. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diseaminated intravascular coagulation; haemorrhapic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meniatis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                          KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                           1 MFGFFCSLVSSLSRWFLWRRILILILILILILILILINPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS
                                                                                                                                                                                                                                                                                                                                       1 MFGFFCSLVSSLSRWFLWRRILLLLLLLLLLLDQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSN 171
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                                                                                                                                                                                                                                                               88.5%; Score 962; DB 7; Length 398; 100.0%; Pred. No. 4.1e-71; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADJ45758 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine tmst2-Fc fusion protein.
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                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 171; Conservative
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                                                                                                                                                                                                                                      Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus
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                                      The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-Fc fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                           KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                       New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
                                                                                                                                                                                                                                                                                                                                                      1 MFGFFCSLVSSLSRWFLWRRILLILLILLILLILLINDPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRKCOCRIGLYYYDPKFPESCRPCTKCPQGIPVLOECNSTANTVCSSSVSN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.5%; Score 962; DB 8; Length 398; 100.0%; Pred. No. 4.1e-71; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse tmst2-receptor splice variant protein.
              Example 4; SEQ ID NO 14; 57pp; English.
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                                                                                                                                                                                                                                                                                    Query Match 88.5
Best Local Similarity 100.
Matches 171; Conservative
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                                                                                                                                                                                                                                                        Sequence 398 AA;
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                                                                                                                                                                                                                         invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
ABW02716
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Claim 13; SEQ ID NO 10; 57pp; English.

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The invention relates to transmembrane decoy-receptor (tmst2) proteins dand their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome present sequence is mouse tmst2-receptor splice variant protein used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                        KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                         KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
                                                                                                                                                                                                                                                                                                                                                       1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease; tmst2-receptor splice variant; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
                                                                                                                                                                                                                                                                                                                                     MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLDQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
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                                                                                                                                                                                                                                                               Length 180;
                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                               87.9%; Score 956; DB 7; I
100.0%; Pred. No. 5.7e-71;
ive 0; Mismatches 0;
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Best Local Similarity 100..
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                                                                                                                                                                                                                               Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SARI/) SARIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2004018544-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
*5555555555555
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                                          in invention treates to a unit in the sequence of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (ALDS), anaemia, autoimmune diseases, cachaxia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-receptor splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                           61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KNCSAGIFVKAPCEIPHTQGQCEKCHPGTPTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory; disease; chromosome mapphing; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunosupdrastitic; antiinflammatory; antiparastitic;
                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
                                                                                                                                                                                                                                                                                                                                                      1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                         1 MFGFFCSLVSSLSRWFLWRRLLILLILLILLILLOPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                     ;
                               relates to a tmst2-receptor polypeptides and the
                                                                                                                                                                                                                                                                                 87.9%; Score 956; DB 8; Length 180;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse tmst2-receptor protein from tmst2-00004-d1 clone.
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 5.7e-71; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 6; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABW02714 standard; protein; 133
                                                                                                                                                                                                            polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUL-2000; 2000US-00612033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0143063P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-874309/81.
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 170; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAD64753.
                                                                                                                                                                                                                                                  Sequence 180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS6627199-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABW02714;
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The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polymucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tunst and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, usiral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tunst2-receptor protein used in the
                                                                                                                                                                                                                                                                                                                                                                                         KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                      KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; tmst2-receptor; tmst2 00004-d1; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmuno disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disease; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclarosasis; isechaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.
                                                                                                                                                                                                                                                                                                                        1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                   Score 748; DB 7; Length 133;
Pred. No. 5.9e-54;
                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                       68.8%; Scor.
100.0%; Pred. No. 5...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ45750 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine tmst2 00004-dl polypeptide.
                                                                                                                                                                     exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JUL-1999; 99US-0143063P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                DRKCQCRIGLYYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                        DRKCQCRTGLYYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 133; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-224390/21.
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                                                                                                                                                                                                    Sequence 133 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SARI/) SARIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
   88888888888888888
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The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-receptor polypeptide clone of the
                                                                                                                                                                                                                                                                                                                                                                          61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                             61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.
                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                              1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                 Gaps
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for screening substances
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                                                                                                                                                                                                                                                Length 133;
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                68.8%; Score 748; DB 8; L
100.0%; Pred. No. 5.9e-54;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor protein inducing differentiation extracellular region only and can be used treatment of bone growth disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .28
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29. .176
/note= "mature protein"
Example 1; SEQ ID NO 6; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 29-31; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW80254 standard; protein; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of protein 7F4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-00099653
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                                                                                                                                                                                                                                                                                                                                                                                                                                         121 DRKCQCRTGLYYY 133
                                                                                                                                                                                                                                                               Best Local Similarity 100.0
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimura N, Toyoshima T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 DRKCQCRTGLYYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-568275/48.
N-PSDB; AAV68046.
                                                                                                                                                                                                                   Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
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                                                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80254;
                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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             The present sequence represents a protein designated 7F4. This protein is scapable of inducing differentiation in osteoblast cells. The protein may be used to screen compounds for the ability to bind to it, for use as ligands, agonists or antagonists and inhibiting or otherwise altering its differentiation inducing activity. Compounds so identified, as well as the protein itself, DNA encoding it, and antibodies to it, may be used in the treatment of diseases of bone growth and osteoblast differentiation,
                                                                                                                                                                                                                                                                                                                                           TEVXAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC 116
                                                                                                                                                                                                                                                                                                                                                                                                             QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSSVSNPRNWLFLLM----- 170
                                                                                                                                                                                                                                                                                                                           TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                         127 RIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
                                                                                                                                                                                                                                                                                           SHVSSLSHWF-----LLLLLLLLLLPVIFAMPESYSPNCPDGEYQSNDVCCKTCPSG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumou: cancer; acquired immune defliciency syndrome; ALDS; aneamia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                                                                                                                           7 SLVSSLSRWFLWRRLLLLLLLLLLLLLLLLVVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel ymkz5-receptor polypeptide useful for treating diseases such as tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                         17;
                                                                                                                                                                                            Length 176;
                                                                                                                                                                                                                            22; Indels
                                                                                                                                                                                            DB 2;
                                                                                                                                                                                            Score 746.5; DB Pred. No. 1e-53;
                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADF57551 standard; protein; 176 AA
                                                                                                                                                                                           68.7%;
75.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1999; 99US-0143137P, 07-JUL-2000; 2000US-00611989.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                           Matches 142; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 IVSVVVFRI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::|| |
---LIVECI 176
                                                                                                                              as bone sarcomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse ymkz5 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-008943/01.
N-PSDB; ADF57550.
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                            Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ZHAN/) ZHANG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2003096355-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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                                                                                                                              such
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Claim 13; SEQ ID NO 8; 57pp; English.

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tumour necrosis factor (TNF) receptor supergene family and nucleic acid diseases encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymkz5 receptor protein.
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                                                                                                                                                                                                                                                                                                                                                                              116
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a transgenic non-human animal having the expression of FW4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agents for the prevention and
                                                                                                                                                                                                                                                                                                                                              67 TFVKAPCEIPHTQGQCEKCHPGTFTEKONYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                                               127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                             26
 invention relates to transmembrane decoy receptor, ymkz5 belonging
                                                                                                                                                                                                                                                                                                                                                                    57 TFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC
                                                                                                                                                                                                                                                                                7 SLVSSLSRWFLWRRLLLLLLLLLLLLLLLDQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                                                                                                                                   SHVSSLSHWF------LLILILINLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic non-human animal with modified expression of 7F4 gene screening remedies for bone or glycolipid metabolism disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes.
                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                 Length 176;
                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                               68.7%; Score 746.5; DB 8;
75.1%; Pred. No. 1e-53;
tive 8; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; SEQ ID NO 2; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADM46623 standard; protein; 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-SEP-2003; 2003WO-JP011545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-2002; 2002JP-00270321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makishima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 IVSVVVFRI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-340227/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | || ::
|---EIVFCI
                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saito H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse 7F4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADM46622
                                                                                                                                                                              Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004026026-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-2004
                                                                                                                                                                                                                                              Matches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADM46623;
                                                                                                                                                                                                                                                                                                               Ŋ
                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kake T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADM4662
                                                                                                                                                                                                                                   Best
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26

99

Gaps

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Length 396;

Score 711; DB 8; Length 39 Pred. No. 2e-50; 5; Mismatches 20; Indels

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acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymk25-human Fc fusion protein.
                                                                                                                                                                                       TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                      TFVXAPCKIPHTQGQCEXCHPGTFTGKDNGLHDCELCSTCDKDQNNVADCSATSDRKCEC 116
                                                                                                                                                            SHVSSLSHWF-----LLLLLLLLLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG
                                                                                                                                      SLVSSLSRWFLWRRLLLLLLLLLLLLLOVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                                                                                     127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSN 171
                                                                                                                                                                                                                                                                                                                                ADM46624 standard; protein; 148
                                                                                      65.4%;
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Mouse 7F4 protein #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-340227/31.
                                                                                   Query Match
Best Local Similarity
Matches 132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saito H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
tes 123; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 AA;
                                                              Sequence 396 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004026026-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-2004
                                                                                                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                         ADM46624;
                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kake T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                    ADM46624
                                                                                                                                                                                                                                                                                                                                 8888888
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                                                                                                                                                                               TFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNWVADCSATSDRKCEC 116
                                                                                                                                                                67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                 RTGLYYYDPKFPBSCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
                                                                                                                                                                                                                                tumour;
                                                                                                                                      56
  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumou cancer; acquired immune deficiency syndrome; ALDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                              for treating diseases such as diseases, cachexia, leprosy,
                                                                                                             7 SLVSSLSRWFLWRRLLLLLLLLLLLLLLLVVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                       Gaps
 treatment of diseases including osteoporosis, obesity and diabetes. present sequence represents the modified mouse 7F4 protein.
                                                                                       17;
                                                              Score 746.5; DB 8; Length 176; Pred. No. 1e-53;
                                                                                     22; Indels
                                                                                      8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel ymkz5-receptor polypeptide useful tumor, cancer, AIDS, anemia, autoimmune leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 14; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse ymkz5-human Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                         ADF57557 standard; protein; 396 AA
                                                              68.7%;
75.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2002; 2002US-00193616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999; 99US-0143137P.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                       Matches 142; Conservative
                                                                                                                                                                                                                                                                  187 IVSVVVFRI 195
                                                                                                                                                                                                                                                                                  ::|| |
---LIVFCI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-008943/01.
                                                                                                                                  SHVSSLSHWF-
                                                                          Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003096355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZHAN/) ZHANG
                                       Sequence 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                         12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric.
                                                                                                                                                                                                                 127
                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                          171
                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhang K;
                                                                             Local
                                                                                                                                                                                                                                                                                                                                 RESULT 12
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  ន្តដ្ឋប្ល
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic non-human animal with modified expression of 7F4 gene screening remedies for bone or glycolipid metabolism disorders.
7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ٠.
د.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.8%; Score 682.5; DB 8; larity 78.3%; Pred. No. 1.7e-48; Conservative 8; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 3; SEQ ID NO 3; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ē
                                                                                                                                                                                                                                                                                                                 10-SEP-2003; 2003WO-JP011545.
                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-2002; 2002JP-00270321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Makishima
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUS ) CHUGAI SEIYAKU KK
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106

42

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Gaps

25;

Indels

Length 380;

DB 4; ٠.

ABG09344;

159 121

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43 LHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACIL 102
                                                                                                                                                                                                         107 IHSPRCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACIL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; acquired immune deficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                 Novel ymkz5-receptor polypeptide useful for treating diseases such ar
tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,
leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse ymkz5 receptor from clone ymkz5-00013-g11.
                          Pred. No. 1.5e-36;
                                             0; Mismatches
  Score 542.5;
                                                                                          8 LVSSLSRWFLWRRLLLLLLLLLLLLNLPLQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF57549 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2002; 2002US-00193616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUL-1999; 99US-0143137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 73.6%;
Matches 89; Conservative
49.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                             Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-008943/01.
                                                                                                                                                                                                                                                                         CSTCDK 108
                                                                                                                                                                                                                                                                                                                 CSTCDK 172
                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADF57563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US2003096355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZHAN/) ZHANG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2004
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                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF57549;
                                                                                                                                                                                                                                                                         103
                                                                                                                                                                                                                                                                                                                   167
Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang K;
                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed in diagnostics as expressed sequence tags for identifying expressed activity of (II) as useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and its and its and its and its and its and its protein expression or biological activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic maino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pct_sequences
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         involving aberrant protein expression or biological activity. The bolypeptide and polymuclocide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH
                                                                       61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKPPSSCRPCTKCPQGIPVLQECN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                 STANTVCSSSVSNPRNWLFLLM-----LIVFCI 148
                                                                                                                                  STANTVCSSSVSNPRNRLFLLLSPLSVLIVSVVVFRI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID NO 39703; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Novel human diagnostic protein #9335.
                                                                                                                                                                                                                                                                                            ABG09344 standard; protein; 380 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAS73531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 380 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drmanac RT,
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                                                                              The invention relates to transmembrane decoy receptor, ymkz5 belonging to tumour necrosis factor (TNF) receptor supergene family and nucleic acid sequences encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymkz5 receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 467; DB 8; Length 117;
Pred. No. 7.6e-31;
5; Mismatches 19; Indels
Example 1; SEQ ID NO 6; 57pp; English.
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Search completed: September 9, 2005, 08:53:49 Job time : 599.714 secs

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rei ke

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

9, 2005, 07:09:19; Search time 127.81 Seconds (without alignments) 115.645 Million cell updates/sec September Run on:

US-10-622-407-8

Perfect score:

1087 1 MFGFFCSLVSSLSRWFLMRR......LLSPLSVLIVSVVVFRIIRR 198 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

513545 segs, 74649064 residues Searched:

513545 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

lsgued Patents AA.*
1: /cgn2_6/ptodata/liaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/liaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/liaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/liaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/liaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/liaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
ΩΙ	US-09-612-033B-8 US-09-612-033B-14	US-09-612-033B-10	US-09-612-033B-6	US-U9-411-722-1 US-09-855-266A-1	US-09-411-722-2	US-09-855-266A-2	US-09-290-640-66	US-09-665-615B-66	US-09-855-266A-13	US-08-292-549-6	US-09-006-353A-14	US-09-573-986-14	US-08-804-166-6	US-08-910-991-6	8-09-756-186-6	US-08-804-166-2	US-08-910-991-2	US-09-756-186-2	US-08-804-166-4	US-08-910-991-4	US-09-756-186-4	US-08-804-166-8	US-08-910-991-8	US-09-756-186-8	US-08-050-319B-48
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Query Match Length DB	198	180	133	176	148	148	327	327	123	355	355	355	285	285	285	256	256	256	307	307	307	336	336	336	199
Query Match	100.0	87.9	68.8	68.7	62.8	62.8	20.1	20.1	19.5	19.2	19.2	19.5	19.1	19.1	19.1	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.7	18.6
Score	1087	926	748.	746.5	682.5	682.5	218.5	218.5	212.5	208.5	208.5	208.5	207.5	207.5		203.5	203.5	203.5	203.5	203.5	203.5	203.5	203.5	203.5	202.5
Result No.		m	4" ነ	n vo	7	6 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

Sequence 48, Appl Sequence 2, Appli Sequence 2, Appli Sequence 21, Appli Sequence 21, Appli Sequence 46, Appli Sequence 132, Appli Sequence 13, Appli Sequence 13, Appli Sequence 25, Appli
US-08-465-982-48 US-08-050-119B-2 US-08-465-982-2 US-08-465-982-2 US-08-465-982-57 US-08-828-683A-21 US-08-828-683A-21 US-08-974-022-46 US-08-974-022-46 US-08-974-022-46 US-08-974-186-46 US-08-974-186-46 US-08-975-186-46 US-08-975-186-46 US-08-975-186-46 US-08-975-186-46 US-08-975-186-46 US-08-975-186-46 US-08-975-188C-46 US-08-577-988C-46 US-08-975-986-2
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ALIGNMENTS

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Sequence 8, Application US/09612033B
Sequence 8, Application US/09612033B
Sequence 8, Application US/09612033B
Sequence 8, Application US/09612033B
Sequence 8, Application, Identification, and Characterization of TITLE OF INVENTION: tamet2, a No. 6627199e1 Member of the TNF-Receptor Superfamily TITLE OF INVENTION: tamet2, a No. 6627199e1 Member of the TNF-Receptor Superfamily TITLE OF INVENTION: tamet2, a No. 6627199e1 Member of the TNF-Receptor Superfamily CHRENT APPLICATION NUMBER: US/09/612,033B
CURRENT FILING DATE: 1998-07-09
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 8
IENGTH: 198 180 120 61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120 9 9 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS DRKCOCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLL 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC Gaps ö Length 198; Indels Query Match 100.0%; Score 1087; DB 4; Best Local Similarity 100.0%; Pred. No. 5.9e-93; Matches 198; Conservative 0; Mismatches 0; SPLSVLIVSVVVFRIIRR 198 TYPE: PRT
CRGANISM: Mus musculus
US-09-612-033B-8 61 121 181 g 셤 셤 ò ð ò ð

) Sequence 14, Application US/09612033B Patent No. 6627199 (ABREAL INFORMATION: APPLICANT: Saris, Chris TITLE OF INVENTION: Isolation, Identification, and Characterization of US-09-612-033B-14

181 SPLSVLIVSVVVFRIIRR 198

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Sequence 6, Application US/09612033B

Patent No. 6627199
GENERAL INFORMATION:
APPLICANT: Saris, Chris
APPLICANT: Saris, Chris
TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily.
TITLE OF INVENTION: of Genes
TITLE OF INVENTION: of Genes
TITLE OF INVENTION: 06 6000
TITLE OF INVENTION: 06 6000
TITLE OF INVENTION WHERE: US/09/612,033B
CURRENT APPLICATION NUMBER: US 60/143,063
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR PELICATION WHERE: US 60/143,063
PRIOR FILE PREPARED FOR THE US 60/143,063
PRIOR FILE PRIOR FILE WHERE WHE WHERE WHERE WHE WHERE WH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATF 120
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APPLICANT: Toyoshima, Tomoko
TTLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 06501/040001
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
NUMBER: PSELOR ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.5e-61;
8; Mismatches 22;
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Patent No. 6271366
GENERAL INFORMATION:
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Matches 133; Conservative
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Best Local Similarity 75.1
Matches 142; Conservative
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Patent No. 6627199
GENERAL INFORMATION: 6627199
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
FILE REFERENCE: 01017/35434A
CURRENT FILING DATE: 1090-07-07
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 10
LENGTH: 180
              tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLDVVKFAMLELHSFKCPAGEYWSKDVCC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Fusion protein OTHER INFORMATION: consisting of Mus musculus sequences and OTHER INFORMATION: Immunoglobulin sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.5%; Score 962; DB 4; Length 39 Best Local Similarity 100.0%; Pred. No. 4.6e-81; Matches 171; Conservative 0; Mismatches 0; Indels
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TITLE OF INVENTION: tmst2, a No. 6627199el M.
TITLE OF INVENTION: of Genes
FILE REFERENCE: 01017/354344
CURRENT APPLICATION NUMBER: US/09/612,033B
CURRENT PAPLICATION NUMBER: US 60/143,063
FRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Artificial Sequence
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Matches 170; Conservative
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ORGANISM: Mus musculus
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Best Local Similarity
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OTHER INFORMATION:
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US-09-612-033B-10
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RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
                              67 TFVKAPCEIPHTGGCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
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Pred. No. 1.5e-61;
8; Mismatches 22; Indels 17
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Patent No. 6271366
FRENEAL INFORMATION
APPLICANT: Kimura, Nacki
APPLICANT: Toyoshima, Tomoko
ITITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 06501/040001
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT FILING DATE: 1999-10-01
PRIOR FILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                        APPLICANT: Kimura, Naoki
APPLICANT: Kimura, Naoki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPREMENT 66501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT APPLICATION NUMBER: US 09/411,722
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: PC 9/099653
PRIOR FILING DATE: 1997-04-01
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                            ; Sequence 1, Application US/09855266A; Patent No. 6784284; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 68.7%;
Best Local Similarity 75.1%;
Matches 142; Conservative
                                                                                        187 IVSVVVFRI 195
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171 ---LIVFCI 176
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---LIVECI 176
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ORGANISM: Mus musculus
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61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
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                                                                                                                                                                                                                                                                                                                                                                         99 ACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECN 158
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                                                                                                                                                                                                                                                                               39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD 98
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APPLICANT: Kimura.
APPLICANT: Kimura.
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002; CURRENT APPLICATION NUMBER: US/09/855,266A; CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 1999-10-01; PRIOR PRILING DATE: 1999-10-01; PRIOR PILING DATE: 1999-10-01; PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: US 9/09953; PRIOR FILING DATE: 1999-00-01; PRIOR APPLICATION NUMBER: US 9/099653; NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 STANTVCSSSVSNPRNRLFLLLSPLSVLIVSVVVFRI 195
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                                                                                                                                                                                 Score 682.5; DB 3;
Pred. No. 1e-55;
8; Mismatches 17;
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Pred. No. 1e-55;
8; Mismatches
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 2
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                                                                                                                                                                                     62.8%;
78.3%;
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78.3%;
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                                                                                                                                                                                     Query Match
Best Local Similarity 78.3
Matches 123; Conservative
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Best Local Similarity 78.3
Matches 123; Conservative
                                                                                                               ) ORGANISM: Mus musculus
US-09-411-722-2
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US-09-855-266A-2
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              TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REFERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 65
                                                                                                                                                                                                                                                                                                                                                                                                                72 PCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVADCSATSDRKCQCRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                        |:: | : | : | : | : | | 68 DCKMNGGTPTCAPCTEGREYMDKNHYADKCRRCTLCDEEHGLEVETNCTLTQNTKCKCKP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 GLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLLSPLSVLIV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 PCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVADCSATSDRKCQCRT 128
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                                                                                                                                                                                                                                                                                                                                                                         8 LPLVLAGSQLRVHTQGTNSISESLKLRRRVHBTDKNCSEGLYQGGPFCCQPCQPGKKKVE 67
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APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Watch: Jacqueline
TITLE OF INVENTION: Ancisense Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-0502
CURRENT PELICATION NUMBER: US/09/665,615B
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/290,640
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 179
SOFTWARE: Patentin Ver: 2.0
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                                                                                                                                                                                                                                                          DB 3; Length 327;
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                                                                                                                                                                                                                                                        20.1%; Score 218.5; DB 3; Length 3 30.0%; Pred. No. 1.9e-12; tive 30; Mismatches 74; Indels
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Patent No. 6653133
APPLICANT: Marcusson, Eric G.
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Best Local Similarity 30.0°
Matches 57; Conservative
                                                                                                                                                                                                                                                                                             57; Conservative
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                                                                                                                                                                                          ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-09-665-615B-66
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US-09-665-615B-66
                                                                                                                                                                                                             US-09-290-640-66
                                                                                                                                                                          TYPE: PRT
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61 TCRKEMSQVBISPCQADKDTVCGCKENQPQRYLSETHPQCVDCSPCPNG-TVTIPCKETQ 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 TCDKD--QEMVADCSATSDRKCQCRTGLYY-YDPKFPESCRPCTKCPQGIPVLQECNSTA 161
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; Patent No. 5464938
; GENERAL INFORMATION:
    APPLICANT: Smith, Craig A.
    APPLICANT: Goodwin, Raymond G.
    TITIE OF INVENTION: Isolated Viral Protein TNF Antagonists
    NUMBER OF SEQUENCES: 10
    CORRESPONDENCE ADDRESS:
                                                                                                                                                 Sequence 13, Application US/09855266A

Sequence 13, Application US/09855266A

Sequence 13, Application US/09855266A

GENERAL INFORMATION

TITLEOF INFORMATION

TITLEOF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

TITLEOF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN

TITLEOF INVENTION: NOVELS SCRETORY MEMBRANE PROTEIN

CURRENT APPLICATION NUMBER: US/09/855,266A

CURRENT FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-0-01

PRIOR FILING DATE: 1997-04-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FASTERE for Windows Version 4.0

1 PRIOR FILING DATE: 1997-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,549
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51 University Street
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,330
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182 LVFIYRKYRK 191
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 5. CITY: Seattle
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; ORGANISM: Mus musculus
US-09-855-266A-13
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                                                                                                                                   US-09-855-266A-13
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51; Conservative
; MOLECULE TYPE: protein US-09-006-353A-14
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CRGANISM: Homo sapiens
US-09-573-986-14
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           7 LLILSCIIIINSDITPH----EPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTN 62
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                                                                                                                                                                                                                                                                                                                                                68; Indels
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APPLICANT: WE, YING-FEI
APPLICANT: CENTZ, REINER
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME STREET: 9410 VEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP. 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
                                                                                                                                                                                                                                                                                                         19.2%; Score 208.5; DB 1
33.8%; Pred. No. 1.7e-11;
tive 21; Mismatches 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 ESCRPC---TKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 SGCKACVSQTKCGIGYGVSGH-TPTGDVVCS 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KBY WEST AVENUE
                                           NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2602-A
TELECOMOUNICATION INFORMATION:
TELEPAX: (206) 587-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-006-353A-14
; Sequence 14, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
APPLICANT: WEI, YING-FEI
                     ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 355 amino acide
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                51; Conservative
         FILING DATE: 10/19/92
                                                                                                                                                                                                               ; TYPE: amino acid
; TOPCLIGY: linear
MOLECULE TYPE: protein
US-08-292-549-6
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Best Local Similarity
Matches 51; Conservat
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80 GOCEKCHPGTFTEKDNYLDACILCS-TCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFP 138
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                                                                                                           21 LILLILLILLILLILLINLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEI-PHTQ
                                                         Indels 11; Gaps
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  Length 355;
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APPLICANT: Wei, Ying-Fei
APPLICANT: Gentz, Reiner
APPLICANT: Ruben, Stewen
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488.1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
Query Match
19.2%; Score 208.5; DB 3;
Best Local Similarity 33.8%; Pred. No. 1.7e-11;
Matches 51; Conservative 21; Mismatches 68;
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; Sequence 6, Application US/08804166
; Patent No. 6193972
; GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSE;
ADDRESSEE: ADDRESSE;
ATREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ESCRPC---TKCPQGIPVLQECNSTANTVCS 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09573986
Patent No. 6455040
GENERAL INFORMATION:
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Search completed: September 9, 2005, 09:35:53 Job time: 127.81 secs

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September 9, 2005, 08:34:50; Search time 602.905 Seconds (without alignments) 129.535 Million cell updates/sec
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1 MFGFFCSLVSSLSRWFLWRR......LLSPLSVLIVSVVVFRIIRR 198
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| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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Maximum DB seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence 8, Appli	Sequence 14, Appl	Sequence 10, Appl	Œ	Sequence 1, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli
ΩΙ	. US-10-622-407-8	US-10-622-407-14	US-10-622-407-10	US-10-622-407-6	US-09-855-266A-1	US-10-193-616-8	US-10-802-332-1	US-10-193-616-14	US-09-855-266A-2	US-10-802-332-2	US-10-193-616-6
08	15	15	15	15	σ	14	16	14	δ	16	14
% Query Match Length DB	198	398	180	133	176	176	176	396	148	148	117
% Query Match	100.0	88.5	87.9	68.8	68.7	68.7	68.7	65.4	62.8	62.8	43.0
Score	1087	962	926	748	746.5	746.5	746.5	711	682.5	682.5	467
Result No.	-	7	e	4	S	9	7	80	σ	10	11

Sequence 10, Appl Sequence 3, Appli Sequence 24, Appl Sequence 18, Appl Sequence 66, Appl Sequence 66, Appl	13, 13, 13, 13, 13, 13, 13, 13, 13, 13,	Sequence 14, Appl Sequence 16, Appl Sequence 6, Appli Sequence 15, Appl Sequence 15, Appl Sequence 13, Appl Sequence 13, Appl Sequence 18, Appl Sequence 12, Appl Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 11, Appli
14 US-10-193-616-10 15 US-10-410-012-3 16 US-10-799-345-24 9 US-09-948-018-18 14 US-10-193-616-9 9 US-09-802-6669-66	20 US-11-023-449-23 9 US-09-855-566A-13 16 US-10-802-332-13 16 US-10-748-112-21 9 US-09-899-422-15 9 US-09-899-429A-25 9 US-09-993-429A-25 9 US-09-92-356-15 9 US-09-935-736-15	14 US-10.186 643-14 15 US-10-418 2-42-16 9 US-09-756-186-6 16 US-10-724-226-6 19 US-09-798-799-15 19 US-09-799-799-13 9 US-09-799-799-13 19 US-09-798-799-13 10 US-09-899-429A-18 10 US-09-899-429A-18 10 US-10-724-226-2 16 US-10-724-226-2 16 US-10-724-226-3 16 US-10-724-226-4 16 US-10-724-226-4 16 US-10-724-226-4 16 US-10-724-226-4 16 US-10-724-226-4 16 US-10-724-226-4 16 US-10-724-226-8 16 US-10-724-226-8 16 US-10-724-226-8
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113 114 116 116	2 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	

ALIGNMENTS

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Sequence 8, Application US/10622407

Sequence 8, Application US/10622407

Publication No. US200400185441

Publication No. US200400185441

Publication No. US200400185441

APPLICANT: Saris, Chris

TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

FILE REFERENCE: 01017/354348

CURRENT APPLICATION NUMBER: US/10/622,407

PRIOR APPLICATION NUMBER: US 09/612,033

PRIOR APPLICATION NUMBER: US 09/612,033

PRIOR APPLICATION NUMBER: US 60/143,063

PRIOR FILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0
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100.0%; Score 1087; DB 15; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.2e-87;
Matches 198; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-8
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Sequence 6, Application US/10622407
Sequence 6, Application US/10622407
Publication No. US20040018544A1
GENERAL INFORMATION:
APPLICANT: Saris, Chris
TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
FILE REFERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR PILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                    61 KNCSAGTFVKAPCEIPHTOGOCEKCHPGTFTEKDNYLDACILCSTCDKDOEMVADCSATS 120
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                                                                             87.9%; Score 956; DB 15; Length 180;
llarity 100.0%; Pred. No. 3.6e-76;
Conservative 0; Mismatches 0; Indels (
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Patent No. US20020128435A1
GENERAL INFORMATION:
APPLICANT: Kiundai, Nacki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 66501-040002
CURRENT APPLIANCATION UNDBER: US/09/855, 266A
CURRENT APLIANC DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
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ORGANISM: Mus musculus US-10-622-407-10
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US-10-622-407-6
                                                                                                       al Similarity
170; Conserv
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Best Local Similarity
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                                                                                     Query Match
                                                                                                             Best Local
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| Sequence 14, Application No. US20040018544A1
| Publication No. US20040018544A1
| GENERAL INFORMATION:
| APPLICANT: Saris, Chris
| TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
| TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
| TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
| TITLE OF INVENTION: MUMBER: US/10/622,407
| CURRENT FILING DATE: 2003-07-17
| PRIOR FILING DATE: 1999-07-09
| PRIOR FILING DATE: 1999-07-09
| PRIOR FILING DATE: 1999-07-09
| NUMBER OF SEQ ID NOS: 15
| SEQ ID NO 14
| LENGTH: 398
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TITLE OF INVENTION: IDSUATION, IDENTIFICATION, AND CHARACTERIZATION OF TWST2, A NOVEL
TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
FILE REPERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT PILING DATE: 2003-07-17
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHING DATE: 2000-07-07
LENGTH: 180
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                                  121 DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLL 180
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     DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Fusion protein OTHER INFORMATION: consisting of Mus musculus sequences and OTHER INFORMATION: Immunoglobulin sequences
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                                                                                                                                     181 SPLSVLIVSVVVFRIIRR 198
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US-10-622-407-10
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9

Gaps

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Indels

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CENERAL INTEGRAL Sharp, Ke
TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
FILE REFERENCE: 01017/35551A
CURRENT APPLICATION WUMBER: US/10/193,616
CURRENT APPLICATION NUMBER: US/09/611,989
PRIOR APPLICATION NUMBER: US 60/143,137
PRIOR FILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/10193616
Publication No. US20030096355A1
GENERAL INFORMATION:
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TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: ymkZ5, a novel
TITLE OF INVENTION: ymkZ5, a novel
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
FILE REFERENCE: 01017/35551A
CURRENT APPLICATION NUMBER: US/10/193,616
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,137
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,137
PRIOR FILING DATE: 1999-07-07
SPRIOR FILING DATE: 1599-07-07
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                             Length 176;
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                                                                                                                                                                                                                                                                                                             DB 9;
                                                                                                                                                                                                                                                                                                           68.7%; Score 746.5; DB 9, 75.1%; Pred. No. 9.3e-58; cive 8; Mismatches 22.
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR PILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTESO for Windows Version 4.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.19
Matches 142; Conservative
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US-10-193-616-8
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Best Local
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67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
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TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
CURRENT APPLICATION NUMBER: US/10/802,332
CURRENT FILING DATE: 2004-03-16
PRIOR FILING DATE: 2001-05-14
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1997-04-01
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Best Local Similarity 75.1%; Pred. No. 9.3e-58;
Matches 142; Conservative 8; Mismatches 22
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                         Sequence 1, Application US/10802332 Publication No. US20040152879A1 GENERAL INFORMATION:
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---LIVECI 176
187 IVSVVVFRI 195
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                                                                                                                                                         65.4%; Score 711; DB 14; Length 396; 80.0%; Pred. No. 2.8e-54; ive 5; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KIMURA, Naoki
APPLICANT: Toyoshima, Tomoko
ITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 66501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT PILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1999-40-01
PRIOR FILING DATE: 1999-44-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1997-04-01
SPRIOR FILING DATE: 1997-04-01
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                                                                                      OTHER INFORMATION: ymkz5-Fc fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/09855266A ; Patent No. US20020128435A1
                                                                                                                                                                               Best Local Similarity 80.0 Matches 132; Conservative
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                     TYPE: PRT
ORGANISM: Mus musculus
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US-10-193-616-14
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LENGIH: 396
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Sequence 2, Application US/10802332; Publication No. US20040152879A1; GENERAL INFORMATION: APPLICANT: Kimura, Naoki; APPLICANT: Toyoshima, Tomoko

US-10-802-332-2

RESULT 10

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67 TPVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
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TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/10/802,332
CURRENT FILING DATE: 2004-03-16
PRIOR APPLICATION NUMBER: US/09/855,266
PRIOR APPLICATION NUMBER: US/09/855,266
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1998-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
SOPTWARE: FASELSEQ for Windows Version 4.0
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Pred. No. 2.3e-33;
5; Mismatches 19;
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73.6%;
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Best Local Similarity 73.69
Matches 89; Conservative
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Best Local Similarity 78.3%
Matches 123, Conservative
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72 PCEIPHTOGOCEKCHPGTFTEKDNYLDACILCSTCDKD--OEMVADCSATSDRKCQCRTG 129
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                                                                                                                                                                                                                                                                                                                                                                                            131 OFORYLSETHFOCYDCSPCFNG-TVTIPCKETONTVCNCHAGFFLRESECVPCSHCKKNE 189
                                                                                                                                                                                                                             72 PCEIPHTGGGCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
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                                                                                                                                                        11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKVVHSKNNSICCTKCHKGTYLVS
                                                                                                                          21 LILLILLILLING-----PLQVKFAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFVKA
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                   Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/10799345

Sequence 24, Application US/10799345

Publication No. US20040209316A1

GENERAL INFORMATION:

APPLICANT: Caristopher T. Ritchlin

APPLICANT: Edward Schwarz

TITLE OF INVENTION: Methods and Compositions Related to

TITLE OF INVENTION: Methods and Compositions Related to

TITLE OF INVENTION: MORPHER 108/100/102

CURRENT PEPLICATION NUMBER: 108/10/799,345

CURRENT FILING DATE: 2004-03-12

PRIOR FILING DATE: 2004-03-14

PRIOR FILING DATE: 2003-03-14
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                          130 LYY-YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS--
                20.8%; Score 226; DB 15; 27.4%; Pred. No. 1.4e-11; iive 27; Mismatches 81;
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SOFWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 454
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; Patent No. US20020150977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                   Query Match
Best Local Similarity 27.4%
Matches 58; Conservative
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US-09-948-018-18
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Sequence 3. Application US/10410012;
Publication No. US2003022827641
GENERAL INFORMATION:
APPLICANT: Pitossi, Fernando J
APPLICANT: Pitossi, Fernando J
APPLICANT: Pitossi, Fernando J
TITLE OF INVENTION: In the substantia nigra and a new model for Parkinson's disease;
TITLE OF INVENTION: In the substantia nigra and a new model for Parkinson's disease;
TITLE OF INVENTION NUMBER: US/10/1410,012
CURRENT APPLICATION NUMBER: US/60/370,974
PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 DCPSPGRDTVCRECEKGTFTASQNYLRQCLSCKTCRKEMSQVEISPCQADKDTVCGCKEN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 PCBIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 QFQRYLSETHFQCVDCSPCFNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
                                                                                                                                                                                                                                                    TITLE OF INVENTION: Isolation, Identification, and Characterization of TITLE OF INVENTION: ymk25, a novel
TITLE OF INVENTION: ymk25, a novel
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
FILE REFERENCE: 0.017/35551A
CURRENT APPLICATION NUMBER: US/10/193,616
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/611,989
PRIOR PILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,137
PRIOR PILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 10
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCTKCHKGTYLVS 70
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                                                                                                                                                                           ; Sequence 10, Application US/10193616; Publication No. US20030096355A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: TNFR1
US-10-193-616-10
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127 R 127
                                               117 9 117
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US-10-193-616-10
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LENGTH: 454
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GENERAL INFORMATION:
APPLICANT: Theill et al
TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
FILE REPERBURE: 0101/37677
CURRENT APPLICATION NUMBER: US/09/948,018
CURRENT FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: US 60/230,191
PRIOR FILING DATE: 2000-09-05
SOFTWARE: Patentin version 3.1
SEQ ID NO 18
LENGTH: 204
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182 LVFIYRKYRK 191
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CRCANISM: Mus musculus
US-09-948-018-18
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Search completed: September 9, 2005, 09:55:17 Job time : 603.905 secs

GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Run on:

9, 2005, 06:50:20 ; Search time 143.524 Seconds September

(without alignments) 132.737 Million cell updates/sec

US-10-622-407-8

1087 1 MFGFFCSLVSSLSRWFLWRR......LLSPLSVLIVSVVVFRIIRR 198 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		J			SUMMARIES	
Result No.	Score	Query Match	* Query Match Length	DB	ID	Description
1	226	20.8	454	-	GOMST1	tumor necrosis fac
8	218.5	20.1	327	~	A46484	
ю	212.5	19.5	461	Н	GQRTT1	tumor necrosis fac
4	210	19.3	324	~	JC2395	Fas antigen precur
S	201.5	18.5	348	~	T28623	hypothetical prote
9	201.5	18.5	349	~	D36858	ote
7	201.5	18.5	349	7	D72175	rotein - v
c o	201.5	18.5	455	-	GQHUT1	sis
6	200.5	18.4	461	7	JC4302	tumor necrosis fac
10	188	17.3	427	Н	GOHUN	nerve growth facto
11	186.5	17.2	271	7	S12783	OX40 antigen precu
12	183.5	16.9	335	7	A40036	
13	180.5	16.6	651	~	JC7705	death receptor-6 -
14	176.5	16.2	416	-	JN0006	nerve growth facto
15	175	16.1	314	~	137383	FAS soluble protei
16	175	16.1	425	Н	A26431	ve growth
17	173.5	16.0	325	7	B43692	T2 protein - rabbi
18	173.5	16.0	461	Н	A35356	tumor necrosis fac
19	167.5	15.4	326	-	GQVZML	T2 protein - myxom
20	162	14.9	272	7	I48700	prote
21	158.5	14.6	435	7	154182	r necr
	157.5	14.5	260	٦	A46517	CD27 antigen precu
	156	14.4	474	(7)	B38634	tumor necrosis fac
24	151.5	13.9	250	П	A49053	CD27 antigen precu
25	151.5	13.9	459	7	I48854	murine t
26	151	13.9	595	N	A42086	
27	143	13.2	277	7	137552	olog -
28	126	11.6	1790	Н	MMFFB1	-1
53	123	11.3	256	~	B32393	T-cell antigen 4-1

B cell-associated	membrane glycoprot	lymphocyte activat	laminin alpha 5 ch	laminin B2t chain	perlecan precursor	laminin beta-2 cha	epidermal growth f	heparan sulfate pr	laminin gamma-1 ch	alpha-2-macroglobu	hypothetical prote	serine proteinase	laminin beta-1 cha	major surface-labe	laminin gamma 2 ch
A46476	JC5486	138426	T10053	A44018	A38096	MMRTS	JC4387	S18252	MMHUB2	\$25111	T25933	S34583	MMMSB1	A35502	000698
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305	493	255	3635	1193	4391	1801	1339	3707	1609	4545	1372	1548	1786	713	1192
11.2	11.2	11.1	11.0	10.7	10.7	10.5	10.5	10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.1
122	121.5	120.5	119.5	116	116	114.5	114	112	111.5	111.5	111	111	111	110.5	110
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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necrosis factor receptor 1 precursor - mouse

NyAlternate names: tumor necrosis factor receptor, 55K C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004 C;Accession: A38634; B40054; Si6677; S19021; 154532; 157826 R;Lewis, M; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, B. Apric. Nall. Acad. Sci. U.S.A. 88, 2830-2834, 1991 A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A; MOLECULE type: mRNA
A; Residues: 1.454 < LLEN>
A; Residues: 1.454 < LLEN>
A; Residues: 1.454 < LLEN>
A; Cross-references: UNIPPROT: P25118; GB: M60468; NID: g199825; PIDN: AAA39751.1; PID: g199826
R; Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
Mol. Cell. Biol. 11, 3020-3026, 1991
A; Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for A; Reference number: A40254; MUID: 91246168; PMID: 1645445

A; Molecule type: mRNA A; Residues: 1-54 <CO2> A; Cross-retences: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826 A; Cross-retences: GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826 B; Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldma Bur. J. Immunol. 21, 1649-1656, 1991 Bur. J. Immunol. 21, 1649-1656, 1991 A; Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis A; Reference number: S16677; MUID:91285014; PMID:1647956

receptor type b. A; Molecule type: mRNA
A; Meadidues: 1-494 < GARA.
A; Readidues: 1-494 < GARA.
A; Cross-references: EMBL: X59238; NID: G53578; PIDN: CAA41922.1; PID: G53579
R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
R; Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
A; A; A34-340, 1991
A; Title: Molecular Coloning and expression of the mouse Inf receptor type
A; Reference number: S19021; MUID: 92039815; PMID: 1657766

A;Accession: S19021

A; Molecule type: mRNA A; Residues: 1-454 <ROT>

Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849

Immunogenetics 39, 450-451, 1994 A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell l A;Reference number: I54532; MUID:94245292; PMID:8188324

A; Accession: 154532

A;Status: translated from GB/EMBL/DDBJ A;Molecule type: mRNA

A; Residues: 1-454 < RES>

A;Cross-references: GB:L26349; NID:g430732; PIDN:AAA59361.1; PID:g430733
R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
Mol. Immunol. 30, 165-176, 1993
A;Title: Genomic organization and promoter function of the murine tumor necrosis factor A;Reference number: 157826; MUID:93156721; PMID:8381516

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190 ECMKLCLPPVANVTNPQDSGTAVLLPLVIFLGLCLLFFI 228
                     F;44-79/Domain: NGF receptor repeat homology <NGF>
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182 LVFIYRKYRK 191
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Best Local Similarity
Matches 57; Conserva
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A; Residues: 1-461 < HIM>
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A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-393, 03, 435-454 «RE2>
A;Cross-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Coment: This protein is one of two distantly related receptors for both TNF-alpha (cs C;Genetics:
C;Genetics:
A;Gene: TNFR-2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 210/1; 248/1; 257/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolocy (S,Gywords: cytokine receptor; duplication; glycoprotein; receptor; transmembrane protein F;120-454/Pomain: signal sequence #status predicted <STG>F;30-212/Domain: NGF receptor repeat homology <NG1>F;30-212/Domain: NGF receptor repeat homology <NG3>F;127-167/Domain: NGF receptor repeat homology <NG3>F;127-167/Domain: NGF receptor repeat homology <NG3>F;127-167/Domain: Tansmembrane #status predicted <NEM>F;213-235/Domain: intracellular #status predicted <NEM>F;213-235/Domain: transmembrane #status predicted <NEM>F;213-235/Domain: intracellular #status predicted <NEM>F;213-235/Domai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 DCPSPGRDTVCRECEKGTFTASQNYLRQCLSCKTCRKEMSQVEISPCQADKDTVCGCKEN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PCEIPHTQGQCEKCHPGTFTEXDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 OFORYLSETHFOCVDCSPCFNG-TVTIPCKETONTVCNCHAGFFLRESECVPCSHCKKNE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCTKCHKGTYLVS 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLLLLLLLLLLLNL-----PLQVKFAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFVKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.8%; Score 226; DB 1; Length 454; 27.4%; Pred. No. 7.4e-10; ive 27; Mismatches 81; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 LYY-YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
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Best Local
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R;Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M DNA Cell Biol. 9, 705-715, 1990
A;Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A;Reference number: A36555; MUID:91090841; PMID:1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-trees: UNITROT: P22334, GB: M63122, NID: 9207361; PIDN: AAA42256.1, PID: 9207 G, Cross-trees: UNITROT: P22334, GB: M63122, NID: 9207361; PIDN: AAA42256.1, PID: 9207 G; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) G; Superfamily: tumor necrosis factor receptor type I (TNFRI); NGF receptor repeat hom C; Keywords: duplication; glycoprotein; receptor; transmembrane protein F;1-29/Domain: signal sequence #status predicted <SIG>F;30-21/Domain: status predicted <SIG>F;30-21/Domain: extracellular #status predicted <EXT>F;30-21/Product: tumor necrosis factor binding protein #status predicted <TBP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 PCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 QFQRYLSETHFQCVDCSFCFNG-TVTIPCKEKQNTVCNCHAGFFLSGNECTPCSHCKKNQ 189
                                                                                                                                                                                                                                                                                                                72 PCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVADCSATSDRKCQCRT 128
                                                                                                                                                                                                                                                                                                                                                            129 GLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVLIV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71
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                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumor necrosis factor receptor 1 precursor - rat
N;Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
                                                                                                                                                        ----CPAGEYWSKDVCCKNCSAGTFVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 LLLLLLLLLLLLLLLN-----PLQVKFAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFVKA
                                                                                                                                                                                                                                    8 LPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCQPCKKKVE
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F;44-126/Domain: NGF receptor repeat homology sNG2>
F;127-167/Domain: NGF receptor repeat homology sNG3>
F;128-204/Domain: NGF receptor repeat homology sNG3>
F;168-204/Domain: NGF receptor repeat homology sNG4>
F;121-234/Domain: transmembrane #status predicted <NEM>
F;235-461/Domain: intracellular #status predicted <NEM>
F;354-151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                    29;
        Length 327;
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                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86;
DB 2;
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26.0%; Pred. No. 7.6e-09;
                                                Pred. No. 2.1e-09
                                                                                30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 31; Mismatches
    20.1%; Score 218.5;
                                                                                                                                                        32 LPLQVKFAMLELH-----SFK----
                                            30.08;
                                        Local Similarity 30.0%
nes 57; Conservative
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A; Residues: 1-349 <KOL>
A; Residues: 1-349 <KOL>
A; Cross-references: EMBL:K67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A; Cross-references: Etrain India-1967, isolate Ind3
A; Experimental source: strain India-1967, isolate Ind3
B; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchlev, L.S.
B; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchlev, L.S.
A; Shchelkunov, S.N.; Blinov, V.M.; Sandakhchlev, L.S.
A; Title: Genes of variola and vaccinia viruses necessary to overcome the host protective A; Reference number: S32385; MUID:93202281; PMID:8384129
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F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 CDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN 162
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                                                                                                                                                                                                                                           47 KCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCS-T 105
                                                                                                                                                                                                        162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D36858; S46888; S32385; S35987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 KKKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGR
                                                                                                                                                                                                            106 CDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPC---TKCPQGIPVLQECNSTAN
                                                                                                         Gapa
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7;
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   Indele
   55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.5%; Score 201.5; DB 2 35.5%; Pred. No. 4.1e-08; iive 18; Mismatches 55
       Mismatches
       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Riblinov, V.M.
submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X69198
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Best Local Similarity 35.55
Matches 44; Conservative
       Conservative
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A; Residues: 31-168 <SHC>
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                                                                                                                                                                                                                                                                                                                                              163 TVCS 166
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A; Status: preliminary
A; Molecule type: DNA
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          44;
          Matches
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                                                                                                                                                              ran antigen precursor - ran Cypecies: Rattus norvegicus (Norway rat)
C; Species: Rattus norvegicus (Norway rat)
C; Date: 20-Peb-1995 #sequence_revision 20-Peb-1995 #text_change 09-Jul-2004
R; Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Bjochem. Biophys. Res. Commun. 198, 666-674, 1994
A; Reference number: JC2395; MUID: 94128114; PMID: 7507668
A; Reference number: JC2395; MUID: 94128114; PMID: 7507668
A; Residues: J-324 «KIM»
A; Residues: J-324 «KIM»
A; Residues: Last »
A; Residues: Last
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hypothetical protein G2R - variola major virus

C;Species: variola major virus

C;Species: variola major virus

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T28623

R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993

A;Title: Potential virulence determinants in terminal regions of variola smallpox virus

A;Reference number: Z20488; MUID:94088747; PMID:8264798

A;Accession: T28623

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
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A;Coss-references: UNIPROT: P34015; EMBL: L22579; NID: g623595; PIDN: AAA60933.1; PID: g4391
A;Cross-references: UNIPROT: Bangladesh 1975
C;Superfamily: TWP-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 SAGTFVKAPCEIPHTQGQCEKCHPGT----FTEKDNYLDACILCSTCDKDQ--EMVADCS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATSDRKCOCRTGLYYYDPKFPESCRPCTKCPQGI-PVLQECNSTANTVCSSSVSNPRNRL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 19.3%; Score 210; DB 2; Local Similarity 29.4%; Pred. No. 9.1e-09; Nes 57; Conservative 30; Mismatches 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLLLSPLSVLIVSV 190
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                                                                                                                                                   Fas antigen precursor - rat
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A;Molecule type: protein
A;Readidues: 41-45 cRno.
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosch. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purifie
A;Reference number: JC2404; MUID:95128033; PMID:7765720
                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Rededues: 30-38; 41-23, X', 55-79, XX', 82-94, NK'; XX', 100-104; 107-128; 162-167, X', 16
A; Redidues: 30-38; 41-23, X', 55-79, XX', 82-94, NK'; XX', 100-104; 107-128; 162-167, X', 16
A; Note: the purified protein, called tumor necrosis factor binding protein, is a solu
R; Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A; Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of
A; Reference number: A38281; WUID:91017509; PMID:2170974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-455 < GRA>
A; Cross-references: GB:M37764
A; Cross-references: GB:M37764
A; Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 4; Note: the authors translated the codon TGG for residue 37.1 as Thr, AAG for residue 8; Nophar, Y; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtm EMBO J. 9, 3269-3278, 1990
A; Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-455 kNOP>
A,Residues: 1-455 kNOP>
A,Cross-references: EMBL:X55313; NID:g37223; PIDN:CAA39021.1; PID:g37224
A,Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends R;Kemper, 0.; Wallach, D.
Gene 134, 209-216, 199-
A,Title: Cloning and partial characterization of the promoter for the human p55 tumor A,Reference number: JT0758; MUID:94085779; PMID:8262379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-13 «KEM»
K;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
E;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequal-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
A;Residues: 41-43,'X',45-53,'X',55-57 <SEC>
A;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Frigation Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis fa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Riolëson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G. Bur. J. Haematol. 42, 270-275, 1989
A; Title: Isolation and characterization of a tumor necrosis factor binding protein fr A; Reference number: A60594; MUID:89171156; PMID:2924890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule 41-43./X',45-53,'V',55-57,'XK',60 <OLS>
A,Roperimental source: renal failure patient urine
R,Engelmann, H.; Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1331-1354, 1990
A;Title: Two tymor necrosis factor-binding proteins purified from human urine. Eviden
A,Fteference number: A35010; MUID:90110215; PMID:2153136
A,Title: Molecular cloning and expression of human and rat tumor necrosis factor rece
A,Reference number: A36555, MUID:91090841, PMID:1702293
                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-455 <HIM>
A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             le form of the receptor.
A;Reference number: S12057; WUID:91006021; PMID:1698610
A;Accession: S12057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 41-60 <GAT>
A;Experimental source: cancer patient serum
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NyAlternate names: P55 tumor necrosis factor receptor; TWP receptor type 1

NyAlternate names: P55 tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A38208; A34899; A34909; A36555; C38555; A38281; S12057; JT0758; A60231; A38

R;Ruchs, P; Strehl, S; Dworzak, M; Himmler, A; Ambros, P.;

C;Accession: A38208

A;Ttle: Structure of the human TWP receptor 1 (p60) gene (TNRF1) and localization to ch

A;Accession: A38208

A;Melerence number: A38208; MUID:9225049; PMID:1315717

A;Accession: A38208

A;Molecule type: DNA

A;Reference number: A38208; MUID:9225049; PMID:1315717

A;Cross-references: UNIPROT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:A

A;Residues: 1-455 <PUC>
A;Cross-references: UNIPROT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:A

A;Residues: 1-455 <PUC>
A;Cross-references: GB:M34809; MUID:9232584; PMID:2158862

A;Molecule type: maxA,
A;Residues: 1-455 <LOB

A;Reminata : Disputation of the 
                                                              GZR protein - variola minor virus (strain García-1966)
C; Species: variola minor virus
C; Species: variola minor virus
C; Species: variola minor virus
C; Species: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
C; Accession: D72175
R; Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998
A; Description: Analysis of the complete coding sequence of DNA of alastrim variola minor A; Reference number: A72150
A; Accession: D72175
A; Accession: D72175
A; Residues: 1-349 <SHC>
A; Residues: 1-349 <SHC>
A; Residues: 1-349 <SHC>
A; Residues: 1-349 <SHC>
A; Cfonse-references: UNIPROT:P34015; GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G58307, A; Experimental source: strain Garcia-1966
C; Genetics:
A; Gene: G2R
C; Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 201.5; DB 2
; Pred. No. 4.1e-08;
18; Mismatches 55
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35.5%;
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Best Local Similarity
Matches 44; Conserv
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Molecule type: mRNA
1,Robidues 1.427 - 3.00H.
1,Robidues 1.427 - 3.00H.
1,Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
1,Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
1,Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.;
1,Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
1,Reference number: A60204; MUID:87085574; PMID:3025363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 29-31, "T', 33-42, "TT', 45-46, "TX', 50-51, "XX', 54-56 <MAR>
A; Residues: 29-31, "T', 33-42, "TT', 45-46, "TX', 50-51, "XX', 54-56 <MAR>
A; Experimental source: melanoma cell line A875
A; Note: this sequence has been corrected by a note added in proof to follow the nucleotic R; Vissavajihala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajihala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajihala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajihala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vices vice and provided the correction of the correc
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C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
E;1.28/pomain: signal sequence #status predicted <SIG>
F;29-427/Product: nerve growth factor receptor #status experimental <NAT>
F;29-550/Domain: extracellular #status predicted <EXT>
F;32-55/Domain: NGF receptor repeat homology <NGI>
F;67-108/Domain: NGF receptor repeat homology <NGI>
F;109-147/Domain: NGF receptor repeat homology <NGI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the nerve growth factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 PCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTC--DKDQEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                     21 LILLILLILLILLINL-PLQVKFAML----ELHSFKCPAGEY---WSKDVCCKNCSAGTFVKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C.Accession: A25218; A60204; S21689; IS7638
R.JOhnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207 C;Comment: This receptor is found on sensory and sympathetic neurons, on C;Comment: The cysteline-rich region of the extracellular domain may form C;Comment: This protein is thought to form a high-affinity receptor when C;Comment: This receptor undergoes both N- and O-linked glycosylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nerve growth factor receptor precursor, low affinity [validated] - human N;Alternate names: NGF receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell 47, 545-554, 1986
A;Title: Expression and structure of the human NGF receptor.
A;Reference number: A25218; MUID:87051725; PMID:3022937
A;Accession: A25218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 LY--YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 QYRKYWSETLFQ-CLNCSLCPNG-TVQLPCLEKQDTICN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Mecule type: protein
A;Residues: 183-208 <VIS>
R;Sehgal, A.; Patil, N.; Chao, M.
Mol. Call. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the A;Title: A constitutive promoter WID:89096903; PMID:2850481
                 66-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ
                                   30.8%; Pred. ....
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                                                                                                                 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Map position: 17q21-17q22
                                               Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-22 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: I57638
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Canelli S. Darinkin S. Carlon S. 
A;Accession: JC2404
A;Molecule type: protein
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
C;Comment: a source: urine
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-461 <SUT>
A;Cross-references: UNIPROT:P50555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g11417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 29-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JC4302; PC4093
R;Suter, B.; Pauli, U.
Gene 163, 263-266, 1995
A;Title: Cloning of the CDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JC4302; MUID:96011645; PMID:7590278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 LLLLLLLLLLLLVPLQV-----KFAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                predicted <MAT>
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P;1-29/Domain: signal sequence #status predicted <SIG>
P;30-461/Product: tumor necrosis factor receptor p55 #status predicted <WAT P;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
P;44-194/Domain: NGF receptor repeat homology <NG1>
P;84-126/Domain: NGF receptor repeat homology <NG1>
P;211-231/Domain: transmembrane #status predicted <TWM>
P;361-447/Domain: signal transduction #status predicted <SIT>
P;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGLY-YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNOYRHYWSENLFOCFNCSLCLNG-TVHLSCOEKONTVCT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Accession: PC4093
A,Molecule type: protein
A,Residues: 1-7 <SU2>
A,Experimental source: kidney cell line 15
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.5%;
30.6%;
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Matches

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neuroblastoma c part or all of it associates w

DB 2; Length 461;

18.4%; Score 200.5;

Query Match

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A;Cross-references: EMBL:X63717; NID:g28741; PID:g28742
R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; R;
J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a memb
A;Reference number: A38142; MUID:92268122; PMID:1375228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GDB:132671; OMIM:134637
A;Map position: 10q24.1-10q24.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom(C;Superfamily: tumor necrosis factor receptor ransmembrane protein
F;1-16/Domain: supprais; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>
F;85-128/Domain: NGF receptor repeat homology <NG4>
                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P25445; GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor family, belo
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C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom
A; Reference number: A40036; MUID:91309137; PMID:1713127
A; Accession: A40036
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 CCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVAD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPR-N 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              death receptor-6 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Dacts: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
C;Daccssion: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochen. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705, MUID:21308433; PMID:11414698
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C;Comment: This receptor, a member of the tumor necrosis factor re
tresia, activates a cell death and/or survival signaling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; not compared with conceptual translation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-134,'Q',136-335 <OBH>
A;Experimental source: SKW6, 4 Cells
A;Note: sequence extracted from NCB1 backbone (NCBIP:103810)
A;Note: in NCB1 backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;174-190/Domain: transmembrane #status predicted <TMM>
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                                                                                                                                                                                                                                                                R;Krammer, P.H.
submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 RLFLLLSPLSVLI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 WLCLLLLPIPLIV 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Molecule type: nucleic acid
A, Residues: 1-134,'Q',136-335
                                                                                                                                                                                                                                                                                                                          A; Reference number: $24543
                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-335 < KRA>
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                                                                                                                                                                                                A;Residues: 1-335 <ITO>
                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
                                                                                                                                                                      A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                             A; Accession: S24543
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$12783

OX40 antigen precursor - rat

N;Alternate names: nerve growth factor receptor homolog
C;Species: Ratuus norvegicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: $21783; $808036
R;Mailett, $3.; Fossum, $5.; Barclay, A.N.
EMBO J. 9, 1063-1069, 1990
A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A;Reference number: $12783; MUID:90214614; PMID:2157591
A;Accession: $12783
A;Molecule type: mRNA
A;Residues: 1-271 < MALA
A;Residues: 1-271 < MALA
A;Residues: 1-271 < MALA
A;Coss-references: UNIPROT:P15725; EMBL:X17037; NID:g57830; PIDN:CAA34897.1; PID:g57831
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted < MAT>
F;20-271/Product: OX40 antigen #status predicted < MAT>
F;211-235/Domain: transmembrane #status predicted < TMM>
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apoptosis-mediating surface antigen Fas precursor - human
Nalternate names: surface antigen APO-1
C;Alternate names: surface antigen APO-1
C;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence revision 17-Jan-1992 #text_change 09-Jul-2004
C;Accession: A40036; S24543; A38142
R;Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 EKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76 PHTQGQ-CEKCHPGTFTEKDNYLDACILCSTCD--KDQEMVADCSATSDRKCQCRTGLY- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------YDDPKFPESCRPCTKCP-QGIPVLQECNSTANTVCSSSVSNP 172
                                                                                                                                                                                                                                                                                                                                                                 15 LILILILIGVSLGGAKEA-----CPTGLYTHSGECCKACNLGEGVAQPCGA--NQTVC 64
                                                                                                                                                                                                                                                                                                                       24 LLLLLLLLLLNPL-OVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQC 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 FLWRRLLLLLLLLLLLLLLVPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 YVWVQQPTAFILLGLSLGVTVK-----LNCVKDTYPSGHKCCRECQPGHGMVSRCD-52
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                                                                                                                                                                                                                                                                14;
      F;149-189/Domain: NGF receptor repeat homology <NG4>
F;197-248/Region: serine/threonine-rich
F;251-272/Domain: transmembrane #status predicted <TRM>
F;273-427/Domain: intracellular #status predicted <INT>
F;67/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                   Length 427;
                                                                                                                                                                                             17.3%; Score 188; DB 1; Length 42.
34.7%; Pred. No. 4.9e-07;
ive 11; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 RPCTKCPQGIPVLOECNSTANTVC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 EACRVCEAGSGLVFSCODKONTVC 146
                                                                                                                                                                                                                                                             50; Conservative
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Search completed: September 9, 2005, 09:31:38 Job time : 144.524 secs
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A;Residus: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma of c;Comment: This protein is thought to form a high-affinity receptor may form part or all of C;Comment: This protein is thought to form a high-affinity receptor when it associates w C;Superfamily: nerve growth factor receptor; MGF receptor repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NiAlternate names: NGF receptor, low affinity precursor - chicken NiAlternate names: NGF receptor Cispecies: Gallus gallus (chicken) Cispecies: Gallus gallus (chicken) Cibate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 CiAccession: JN00065 A60504 Rilarge, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic A; Li23-1134, 1989 A; Title: Structure and developmental expression of the nerve growth factor receptor in the A; Reference number: JN0006; WUID: 90166579; PMID: 2560385
Fil-21/Domain: Signal sequence #status predicted <SIG>
Fis-2196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
Fi32-350/Domain: transmembrane #status predicted <TMM>
Fi310-475/Domain: death domain #status predicted <DED>
Fi310-475/Domain: death domain #status predicted <DED>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 KSTLRECSPCPDGTFTXHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF--- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 PHTQQQCEKCHPGTFTEKDNYLDACILC-STCDKDQEMVADCSATSDRKCQCRTGLYYYD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                      22 LILLILLILLILLINLPLQVKFAMLELHSFKCPAGEY-----WSKDVCCKNCSAGTFVKAPCEI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 LLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVÇÇKNCSAGTFVKAPCEIPHTQGQCEKCH 86
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A;Cross-references: UNIPROT:P18519
A;Cross-references: UNIPROT:P18519
A;Experimental source: embryonic chick brain
B;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A;Title: Structure and developmental expression of the chicken NGF receptor.
A;Reference number: A60504; MUID:90152140; PMID:2154393
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                                                                                                                                                                                                                                                           16.6%; Score 180.5; DB 2; Length (29.8%; Pred. No. 2.4e-06; tive 27; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                         45; Conservative
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Best Local S:
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C;Accession: 137383
C;Cascino, I.; Flucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are A;Reference number: 137383; MUID:95181785; PMID:7533181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-314 <RES>
A;Cross-references: UNIPROT:P25445; EMBL:Z47993; NID:g728578; PIDN:CAA88031.1; PID:g6955
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 CCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVAD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DSVTYSDTVSATEPCKPCTQCVGLHSMSAPCVESDDAVCRCAYG--YPQDELSGSCKECS 118
87 PG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCT 145
                                                                                                                                                                                                                                                                                                                                                      FAS soluble protein - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mENA
                                                                                                                                                                         119 ICEVGFGLMFPCRDSQDTVC 138
                                                                                                                                    146 KCPQGIPVLQECNSTANTVC 165
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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 8, 2005, 23:31:32; Search time 740.143 Seconds (without alignments) 136.989 Million cell updates/sec Run on:

US-10-622-407-8 1087 1 MFGFFCSLVSSLSRWFLWRR......LLSPLSVLIVSVVFRIIRR 198 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1612378 seqs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9er62 mus musculu	Q9er63 mus musculu	P83626 mus musculu	Q9dfv0 brachydanio	Q7t3m7 gallus gall	-	paralic	Q9df34 brachydanio	Q6dj81 xenopus tro	Q76b99 xenopus lae		097491 ovis aries		Q95185 felis silve	_		Q76b98 xenopus lae		Q6qhfl mus musculu	P25118 mus musculu		Q9tv79 oryctolagus	Q6qhf2 mus spretus	O57119 cowpox viru	Q9xs60 oryctolagus	Q9xs29 oryctolagus	_	O97530 canis famil	O57118 cowpox viru	057120 cowpox viru	O57103 monkeypox v
OI OI	TR22 MOUSE	TR23_MOUSE	TR26 MOUSE	Q9DFV0	Q7T3M7	Q7T3M8	Q800K8	Q9DF34	Q6DJ81	Q76B99	Q6GLZ4	097491	Q678B7	Q95185	TNR6_BOVIN	Q95ND3	Q76в98	Ф6ФНР0	Q6QHF1	TRIA MOUSE	TNR6_PIG	Q9TV79	Q6QHF2	057119	09X860	Q9XS29	TNR6 MOUSE	0975 <u>3</u> 0	057118	057120	057103
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% Query Match Length DB	198	176	204	438	225	410	395	357	321	328	328	327	289	189	323	446	328	440	440	454	332	319	440	347	263	320	327	189	360	326	348
% Query Match	100.0	68.7	29.4	27.9	26.4	26.4	26.2	25.8	24.4	22.7	22.6	22.4	22.0	22.0	21.4	21.4	21.3	20.8	20.8	20.8	20.7	20.6	20.5	20.3	20.1	20.1	20.1	19.9	19.9	19.8	19.8
Score	1087	746.5	320	303	286.5	286.5	284.5	280	265.5	247	246	243.5	239.5	239	233	233	232	226	226	226	224.5	224	223	221	218.5	218.5	218.5	216	216	215.5	215.5
Result No.	1	7	٣	4	ស	9	7	æ	60	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31

057108 monkeypox v 057277 monkeypox v 057101 monkeypox v 057102 monkeypox v 057391 monkeypox v 057312 cowpox viru 057121 cowpox viru 057121 cowpox viru 057122 cowpox viru 057125 cowpox viru 073559 cowpox viru 057354 reatus norv	Q7t2h3 oncorhynchu
057108 057277 057101 057102 057305 057305 057121 067121 067122 CRMB_COWPX 057059 067006 TRIA RAT	<u> 07т2Н</u> 3
44444444444444444444444444444444444444	7
	318
9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	19.5
2112 2113 2113 2113 2113 2113 2113 2113	211.5
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ALIGNMENTS

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Kanal A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Masasi T., Reed J.C., Reed D.J., Raing B.Z., Ringwald M.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setcou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Vurardo R., Wanner L., Wahlestedt C., Wang Y., Watnaba Y., Walls C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazue N.,
Antozane-Kishikawa T., Konno H., Nakamura M., Sakazue N.,
Antozane-Kishikawa T., Konno H., Nakamura M., Sakazue N.,
Antozane-Kishikawa T., Konno H., Nakamura M., Sato K.,
Antozane-Kishikawa J., Materston R., Lander E.S., Rogers J.,
Antono M., Materston R., Lander E.S., Rogers J.,
Antono M., Materston R., Lander E.S., Rogers J.,
Antono M., Materston R., Lander E.S., Rogers J.,
Antozane-Kishikawa M., Materston R., Lander E.S., Rogers J.,
Antono M., Materst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOUG-Q9ER62-2; Sequence=VSP_007648;
ISOUG-COPERING: Ubiquitous.
TISSUE SPECIFICITY: Ubiquitous.
TISSUE SPECIFICITY: Ubiquitous.
CAUTION: Ref.1 (CAC27353) sequence differs from that shown due to erroneous gene model prediction.
CAUTION: Ref.1 (CAC16406) sequence differs from that shown due to a frameshift in position 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apoptosis. Protects cells against TRAIL mediated apoptosis possibly through ligand competition. Cannot induce the NF-kappa-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 2.
Alternative splicing; Glycoprotein; Receptor; Repeat; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUGCELLUAR LOCATION: Type II membrane protein (isoform 1); secreted (isoform 2) (Potential). ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P; 092956; 1JMA.; MGI:1930270; Thfrsf22.

GO:0016021; C:integral tto membrane; NAS.

GO:0004872; F:receptor activity; IDA.

GO:0005569; F:TRAIL binding; IDA.

GO:0005031; F:tumor necrosis factor receptor activity; IDA.

GO:0042981; P:regulation of apoptosis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=1;
IsoId=Q9ER62-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AJ278265, CAC16406.1, ALT_FRAME.
EMBL, AJ276505, CAC2733.1, ALT_SEQ.
EMBL, AY165626, AAN87806.1; -..
EMBL, AX165627, AAN87807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AK012838; BAB28502.2; ALT_INIT.
HSSP; Q92956; 1JMA.
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Pfam; PF00020; TNFR c6; 3.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY046551; AAL05073.1;
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88
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TNFR-Cys 2.

TNFR-Cys 3.

By similarity.
N-linked (GloNac. . . ) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                   DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLL 180
                                                                                                                                                                                                                                                                                                                                       61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                            61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                         1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCC 60
                                                                                                                                                                                                                                                                                         1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                              I (in isoform 2).
/FTId=VSP_007648.
L -> V (in Ref. 2).
L -> C (in Ref. 1; CAC16406).
LLILL -> CVV (in Ref. 1; CAC16406).
EBF8F52961EA9983 CRC64;
                                                                                                                                                                                                                                            100.0%; Score 1087; DB 1; Length 198; 100.0%; Pred. No. 3.4e-85; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                     12 12 L -
24 24 L -
27 30 LLL
198 AA; 22375 MW; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SPLSVLIVSVVVFRIIRR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                  SPLSVLIVSVVVFRIIRR 198
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 198; Conservative
   1554
1655
1657
1000
1116
1124
1154
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1158
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60
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103
1106
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144
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CONFLICT
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                         DISULFID
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TR23 MOUSE STANDARD; PRT; 176 AA.

Q9ER63; Q8VHC0;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 23 precursor (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).

Name=Thfrsf23; Synonyms=Dctrailr1, Thfrh1, Thfrsflal1; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Mus musculus (Mouse) NCBI_TaxID=10090;

Lane N., Reik W., Walter J.;
"Sequence and functional comparison in the Beckwith-Wiedemann region:
"implications for a novel imprinting centre and extended imprinting.";
Hum. Mol. Genet. 9:2691-2706(2000). PubMed=12466268; DOI=10.1074/jbc.M210783200; Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE MODELING OF 52-160. STRAIN=129/Sv; TISSUE=Embryonic stem cells; MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691; Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., STRAIN=C57BL/6;

SEQUENCE FROM N.A.

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               117 QIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNWLFLLM----- 170
                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12466268; DOI=10.1074/jbc.M210783200;
PubMed=12466268; DOI=10.1074/jbc.M210783200;
PubMed=12466268; DOI=10.1074/jbc.M210783200;
PubMed=12466268; DOI=10.1074/jbc.M210783200;
PubMed=12466268; DOI=10.1074/jbc.M210783200;
Gong D., Dobles M., Hartig S., Hofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L.C., Tschopp J., Zheng T.S.;
Fladming L.C., Tschopp J., Zheng T.S.;
Fladming L.C., Tschopp J., Zheng T.S.;
Fladming L.C., Tachopp J., Jecgin (Potential).
J. Biol. Chem. 278:5444-5454(2003).
I. TISSUE SPECIFICITY: Expressed in thymus and spleen. Detectable levels in lung.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND 3D-STRUCTURE MODELING OF
                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 26 precursor (TNF
                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Potential.
Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 3.
Cys-rich.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY165628; AAN87808.1; -.
MGD; MGI:2651928; Thfref26.
Interpro; IRPN C6:
Pfam; PF00020; TNFR C6; 3.
SWART; SM00208; TNFR; 3.
PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 2.
Glycoprotein; Receptor; Repeat, Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          superfamily member 26.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                                                                                                                                                            204 AA
                                                                                                                                                                                                                                                                       Synonyms=Tnfrh3;
                                                                                                                                                            STANDARD;
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204
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1126
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1103
                                                187 IVSVVVFRI 195
                                                                            171 ---LIVFCI 176
                                                                                                                                                                                                                                                        NCBI TaxID=10090;
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P83626;
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                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEVKAPCKI PHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHVSSLSHWF------LLLLLLLNLFLPVIPAMPESYSFNCPDGEYQSNDVCCKTCPSG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 SLVSSLSRWFLWRRLLLLLLLLLLLLLDPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GPI-anchor amidated cysteine (Potential).
                                                                                                          Gaps
Burkly L.C., Tschopp J., Zheng T.S.; Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL)."; J. Biol. Chem. 278:5444-5454 (2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00652; TNFR NGFR 1; 3.
PROSITE; PS50050; TNFR NGFR 2; 2.
Glycoprotein; GPI-anchor; LTpoprotein; Receptor; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Removed in mature form (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1930269; Thfref23.

GO; GO:0005515; P:protein binding; IPI.

GO; GO:0005511; P:tumor necrosis factor receptor activity; IDA.

InterPro; IPR001368; TNFR_C6.

Pfam; PF00020; TNFR_C6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumor necrosis factor receptor
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8; Mismatches 22
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TWFR-Cys 3.

TWFR-Cys 3.

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By similarity.
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SMART; SM00208; TNFF
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176 AA;
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Matches 142; Conserv
                                                                                                  SEQUENCE FROM N.A.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                         83 EKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 LELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDAC 100
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                                                                                                                                                                                                                                         4 LRLLLLLGLLLRV--AVCSVNTITLCKIGEFKHENLCCLQCSAGTYLRNPCQENHNKSEC 61
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                                                                                                                                                                                                                                                                                                                                                                                                                             143 PCTKCPQGIPVLQECNSTANTVCSSSVSNP---RNRLFLLLLSPLSVLIVSVVFRII 196
                                                                                                                                                                                                            24 LLILLLLLLLDPLQVKFAMLELHSFK-CPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQC
                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 SEQUENCE FROM N.A.

19 Bobe J., Goetz F.W.;

10 Bobe J., Goetz F.W.;

11 Idjands in the fish ovary.";

11 Ligands in the fish ovary.";

12 Lomp. Biochem. Physiol. B, Comp. Biochem. 129:475-481(2001).

13 EXBL; AR250042; AAG24365.1;

14 EXBL; AR250042; AAG43456.1;

15 EXBL; AR250042; AAG43465.1;

16 GO; GO: O00515; F: Protein binding;

17 GO; GO: O00515; F: Protein binding;

18 GO; GO: O007165; P: Signal transduction; IEA.

18 GO; GO: O007165; P: Signal transduction; IEA.

19 GO; GO: O007165; P: Signal transduction; IEA.

10 GO: GO: O007165; P: Signal transduction; IEA.

11 InterPro; IPR000488; Death.

12 InterPro; IPR001029; Death.

13 InterPro; IPR001029; Death.

14 Expro; IPR001029; TURR. G6.

15 SWART; SM00209; TURR. G6.

16 SWOSTIE; PSS0019; DEATH DOWAIN; I.

17 PROSITE; PSS0019; DEATH DOWAIN; I.

18 PROSITE; PSS0019; DEATH DOWAIN; I.

19 PROSITE; PSS0015; TURR. NGFR.1; 1.

10 PROSITE; PSS0019; TURR. NGFR.2; 2.
126 143 By similarity.
57 N-linked (GIGNAC. ..) (Potential).
136 N-linked (GIGNAC. ..) (Potential).
204 AA; 22708 MW; A35C5177F178C3DD CRC64;
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                                                                                                                                                                   71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                    29.4%; Score 320; DB 1; 37.9%; Pred. No. 1.3e-19;
                                                                                                                                                              31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Danio rerio)
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                                                                                                                                                                67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58; Conservative
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                                                                                                                                          Similarity
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56 RGKCASCTEGRDYTAHANGLEBCLLCRQCKDDQITLRTCTVTSDTBCQCHQG-YFCPABG 114
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"Alternatively spliced variants of Gallus gallus TNFRSF23 are
expressed in the ovary and differentially regulated by cell signaling
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Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Death domain-containing tumor necrosis factor receptor superfamily
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:|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|| | :|
---SSSVSNPRNRLFLLLSPLSVLIVSVVVFRII 196
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InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001369; FURF_c6.
Pfam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN_1.
PROSITE; PS01186; EGF Z; UNKNOWN 1.
PROSITE; PS010652; TNFR_NGFR_1; 1.
PROSITE; PS000505; TNFR_NGFR_1; 1.
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Biol. Reprod. 70:972-979 (2004).
EMBL, AY251409; AAP41834.1; -.
HSSP; O14763; IDU3.
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40662 MW; 1652B4840D9EEDBA CRC64;
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                                     INTERPRO! IPRO01368; TNFR G6.
INTERPRO! IPRO01368; TNFR G6.
INTERPRO! IPRO01368; TNFR G6.
SMART; SM00208; TNFR; 3.
SMART; SM00343; ZNF C2HC; 2.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS500505; TNFR NGFR 1; UNKNOWN 2.
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InterPro; IPR011029; DEATH like.
InterPro; IPR011029; DEATH like.
Fam; PR00531; Death; 1..
Ffam; PF00020; TNFR_c6; 3.
SMART; SM00208; TNFR; 3.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50050; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_1; 3.
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SEQUENCE
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Q9DF34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
Pleuronectoidei; Paralichthyidae; Paralichthys.
NCBI_TaxID=8255;
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                                                                     Bridgham J.T., Johnson A.L.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AX251408, AAP41833.1; -.
HSSP, 014763; 1D03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     410 AA; 46194 MW; 4BFC7C7016C2BA60 CRC64;
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                                                                                                                                                       GO; GO:0005515; F:protein binding; IEA.
GO; GO:000165; P:protein binding; IEA.
GO; GO:000165; P:receptor activity; IEA.
GO; GO:000165; P:signal transduction; IEA.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001689; Death.
InterPro; IPR001699; BGF like.
InterPro; IPR001509; TNFR c6; 3.
SWART; SW00209; TNFR, 3.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN 1.
PROSITE; PS00106; BGF 2; UNKNOWN 1.
PROSITE; PS00106; BGF 2; UNKNOWN 1.
PROSITE; PS00106; INFR NGFR 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 1.8e-16; 26; Mismatches 53
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GO:0005515, F:protein binding; IEA.
GO:0004872; F:receptor activity; IEA.
GO:0007165, P:signal transduction; IEA.
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Dev. Comp. Immunol. 27:365-375(2003).
EMBL; AB080946; BAC65225.1; -.
EMSP; Ol4763; IDU3.
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  NCBI_TaxID=9031;
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SEQUENCE
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79 QGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFP 138
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MEDLINE=20394299; PubMed=10934476; DOI=10.1038/35019592;
MEDLINE=20394299; PubMed=10934476; DOI=10.1038/35019592;
MEDLINE=20394299; PubMed=10934476; DOI=10.1038/35019592;
Stimulation of erythropoiesis by inhibiting a new hematopoietic death receptor in transgenic zebrafish.";
Nat. Cell Biol. 2:549-552(2000).
Nat. Cell Biol. 2:549-552(2000).
HSMB:, AF302789; AAG21396.1; ---
HSSP; Q92956; 1JWA.
ZFIN; ZDB-GENE-030826-5; hdr.
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000165; P:signal transduction; IEA.
                                                                                                                                                                                                                                                               9 RILVILLSSTGVFPQSRIDFGRRTQRDILCSDNQYLNGNNCCLNCPAGTHVKSHCSKSGE
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                                                                                                                                             7;
                                                                                                                                         84; Indels
395 AA; 44304 MW; 8D685A9F74710AE1 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                        DB 2;
                                                                    ch 26.2%; Score 284.5; DB 2
1 Similarity 33.2%; Pred. No. 2.6e-16;
61; Conservative 32; Mismatches 84.
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InterPro; IPR001368; TNFR_C6.
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SEQUENCE
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MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDINE-2388257; PubMed=1.H., Derged J.G., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Parage C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninot P., Mullahy S.J., M. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., A Richards S., Worley K.M., Sodersten E.J., Lu X., Gibbs R.A., Anderson D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G., Marker Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Marker M., Marker M., Schmutz J., Myers R.M., Butterfield Y.S., Marker M., Malak M., Sansha D., Schmutz J., Myers R.M., Schein J.E., Marker M., Marker M., Sansha M., Schmutz J., Myers R.M., Schein J.E., Marker M., Marker M., Schmutz J., Myers R.M., Schein J.E., Marker M., Marker M., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                       66 GTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQ 125
                                                                                                                                                                                                                                                                       60 GTYVKKACAAAAEKGVCAPCEFDTYTEHDHGLLKCISCDKCRIDQETIEKCTSTQNTRCK 119
                                                                                                                                                                                                                                                                                                                                                                        126 CRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVC--SSSVSNPRNRLFLLLSPL 183
                                                                                                                                                                 | : ||:|||||:
2 RYITLLVLLLLNVINAARSHGDLAWAHRSVKORL--SRDVSCREGLEYPHENICCLNCPA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                 20 RILLILLILLILLINL-------PLOVKFAMLELHSFKCPAG-EYWSKDVCCKNCSA
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                      18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus tropicalis (Western clawed frog) (Silurana tropicalis)
                                Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Whole body:

Klein S., Gerhard D.S.;
Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BOOTS302, AAH75302.1, -.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001456; P:signal transduction; IEA.
InterPro; IPR000488; Cytc Feme_BS.
InterPro; IPR011029; DEATH_like.
                             25.8%; Score 280; DB 2; Length 357 32.4%; Pred. No. 5.8e-16; ive 34; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28, 25-0CT-2004 (TrEMBLrel. 28,
  Query Match
Best Local Similarity 32.**,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 SVLIVSVV 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 IVLLACVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGC88957 protein.
Name=MGC88957;
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Pubmed=1466340; DOI=10.1074/jbc.M306217200;

Eubhed=1466340; DOI=10.1074/jbc.M306217200;

Pubmed=1466340; DOI=10.1074/jbc.M306217200;

Tamura K., Noyama T., Ishizawa Y., Ishizawa Y., Ito M.;

Tamura K., Noyama T., Ishizawa Y., Ishizawa Y., Ito M.;

Tamura K., Noyama T., Ishizawa Y., Ito M.;

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Tamura K., Ito M.;

Tamura M.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 SAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 KCQCRTGLYYYDPKFPESCRPCT-KCPQGIPVLQECNSTANTVCSSSVSNPRNRLFLLLS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 FFC-----YQEGNIRCLRC 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 FFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCCKNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 24.4%; Score 265.5; DB 2; Length Local Similarity 34.0%; Pred. No. 9.1e-15; les 65; Conservative 25; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           21E69219ABB34673 CRC64;
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Last annotation update)
Pfam; PF00531; Death; 1.

Pfam; PF00020; TNRR c6; 2.

SMART; SM00005; DEATH; 1.

SMART; SM00008; TNRR; 2.

PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN 1.

PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.

PROSITE; PS00052; TNRR NGRR 1; UNKNOWN 1.

PROSITE; PS00052; TNRR NGRR 1; UNKNOWN 1.

PROSITE; PS00052; TNRR NGRR 2; 2.

SEQUENCE 321 AA; 36225 FW; 21569219ABB34673 C
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PLLLLVLIVVV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 PLSVLIVSVVV 192
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888888888888
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MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschulz S. F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.H., Rubin G.M., Haish F., Datchenko L., Marusina K., Farmer A.H., Rubin G.M., Hong L., Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Millahy S.J., McZwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiching M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A Rachaguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., R., Gonerzation and initial analysis of more than 15,000 full-length human
                                                                                                                     53 YWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQE 111
                                                                                                                                                                                                                       112 MVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTK-CPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                      38 YQAGNIRCLRCPAGTYVEEPCTTRDTKGECIPCHPGSTYSEGPTGLDHCLSCSRCRDDQE
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                       2;
                       Score 247; DB 2; Length 328;
Pred. No. 3.5e-13;
                                                                       49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
BMBL, BC074299; ARH74299; ARH74299; ARH74299.1; --
GO; GO:00004872; F:procein binding; IEA.
GO; GO:0001465; P:signal transduction; IEA.
InterPro; IPR001450; AFe4S_ferredoxin.
InterPro; IPR001489; Death.
InterPro; IPR001489; Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
XDR-M1 protein.
Name=xDR-M1;
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                                                                       21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog)
                    22.7%;
40.0%;
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                 Query Match
Best Local Similarity 40.0%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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NCBI_TaxID=8355;
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Q6GLZ4
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CPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGT-FTEKDNYLDACILCSTC 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                          53 YWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQE 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            112 MVADCSATSDRKCOCRIGLYYYDPKFPESCRPCTK-CPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 EVRPCTATQNAECRCKKGTYCPMDHPCEVCLTCTESCPPGQELHLPCNSTSDSHCGPAES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Lymphocyte;
Takagi M., Takadiahi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011671; BAA37093.1; -.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                        Length 328,
                                                                                                                                                                                                                                                                                                                  Query Match 22.6%; Score 246; DB 2; Length 32
Best Local Similarity 40.0%; Pred. No. 4.3e-13;
Matches 48; Conservative 21; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:apoptosis; IEA.
GO; GO:0006555; P:immune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
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                                                                                                                                                                                                                                                               7938B5F56F9C58E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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InterPro; IPR001368; TNFR_c6.
Pfam; PF00531; Death; 1.
Pfam; PF00020; TNRR_c6; 1.
SMART; SM00006; DBATH; 1.
SMART; SM00006; DBATH; 1.
PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00617; DBATH DOMAIN; 1.
PROSITE; PS00620; TNFR_NGFR_1; UNKNOWN_1.
PROSITE; PS00650; TNFR_NGFR_2; 2.
SEQUENCE 328 AA; 37262 MW; 7938BSF56F9C58E7 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000488; Death.
InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011029; DEATH_like.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00031; Death; IV.
Pfam; PF00020; TNFR_c6; 2.
PRINTS; R000005; DEATH; IV.
SMART; SM00006; DEATH; IV.
PROSITE; PSS0017; DEATH; JONAIN; IV.
PROSITE; PSS0017; DEATH; DONAIN; IV.
PROSITE; PSS0052; TNFR_NGFR_1; UNKNOWN_IV.
PROSITE; PSS0052; TNFR_NGFR_1; UNKNOWN_IV.
PROSITE; PSS0052; TNFR_NGFR_1; Z.
SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ovis aries (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P25445; 1DDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fas protein.
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HSSP; P19438; 1EXT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNR6 BOVIN
                                                                                                                                                                                                                                                                            Receptor.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P51867:
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                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                              84 KCHPGIFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRP 143
DKDQ--EMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 PCSPGTYTGLQNSLRKCLRCSTCSHNEEPKVACSTTSDVQCQCRQG-YYYDPE-SEMCFP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24 LLLLLLLLLLLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCE 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Lymphocystis disease virus - isolate China. Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus. NCBL_TaxID=256729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Duthie S., Nasir L., Eckersall P.D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; U72344; AAB95089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 AA; 32691 MW; 26B6114D4D5D6C3F CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae;
                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 28, Created)
(TrEMBLrel. 28, Last sequence update)
(TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-UUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumour necrosis factor receptor p60 (Fragment)
                                                                                                  CSSSVSNPRNRLFLLLSPLSVLIVSVVVFRIIRR 198
                                                                                                                                                CKGSRSH-TNSLWALLILLLILIFLIIYKVVRR 196
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                                                                                                                                                                                                                                                                            289 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.0%; Score 239.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00208; TNFR; 4.

SMOSITE; PS01186; EGF 2; 2.

PROSITE; PS00505; TNFR NGFR 1; UNKNOWN 2.

PROSITE; PS50050; TNFR NGFR 2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 CTKCPQGIPVLQECNSTANTVC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSNCESSKVKVTTCNRTHDTVC 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AY380826; AAU10940.1; -. InterPro; IPR006209; EGF like. InterPro; IPR001368; TWFR_C6. Pfam; PF00020; TWFR_C6; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78:6982-6994 (2004).
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                                                                                                                                                                                                                                                                         PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
                                                                                                                                                                                                                                                                                                                        25-OCT-2004
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                                              107
                                                                                                  165
                                                                                                                                                164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                      RESULT 13
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 EGPGLDTDCRECENGTFTASENYLRQCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQY 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIPHIQGOCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTGLY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LVLLALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKYIHPQDNSICCTKCHKGTYLYNDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIANE=96226401; PubMed=8634151;
Yoo J., Stone R.T., Beattie C.W.;
Yoo J., Stone R.T., Beattie C.W.;
"Cloning and characterization of the bovine Fas.";
DNA Cell Biol. 15:227-234(1996).
-!- FUNCTION: Receptor for TNFSF6/FASL. The adaptor molecule FADD
recruite scapase-8 to the activated receptor. The resulting death-
inducing signaling complex (DISC) performs caspase-8 proteolytic
activation which initiates the subsequent cascade of caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILILILILILILILILIVPIQVKFAM----LELHSFKCPAGEY---WSKDVCCKNCSAGTFVKAPC
                                                                                                                                                                                                                                                                                                                                                                                                           12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: Contains a death domain involved in the binding of FADD, and maybe to other cytosolic adaptor proteins.
-!- SIMILARITY: Contains 1 death domain.
-!- SIMILARITY: Contains 3 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
25-0CT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 189;
                                                                                                                                                                                                                                                                                                                                                      / Match 22.0%; Score 239; DB 2; Length 18 Local Similarity 35.3%; Pred. No. 1e-12; Les 55; Conservative 19; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                       21420 MW; F3FBE0CE809D7DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 -YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 RYYWSETHFOCLNCSLCLNG-TVOISCKETONTVCT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both (By similarity).
SUBUNIT: Binds DAXX and RIPK1 (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA.
                                                                                                                                                   PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS01186; EGF 2; UNKNOWN 1.
PROSITE; PS00652; TNFR NGFR 1; 3.
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000345; CytC heme BS.
InterPro; IPR001345; CytC heme BS.
InterPro; IPR001368; TNFR_C6.
Pfam; PF00020; TNFR_C6; 3.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=TNFRSF6; Synonyms=APT1, FAS;
                                                                                                                                                                                                   PROSITE; PS50052; TNFR NGFR 1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                         189 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine)
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                                                                                                                                                                                                                                                                                  189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CD95 antigen)
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 VKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTOGOCEKCHPGT-FTEKD 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 LKLNITEANS--CQEGLYREHQFCCQPCPPGKKKNGDCKRDGDTPECVLCSEGNEYTDKS 92
                                                                                 R InterPro; IPR004048; Death.
R InterPro; IPR004068; Death.
R InterPro; IPR001029; DEATH_like.
R InterPro; IPR001029; DEATH_like.
R InterPro; IPR001063; FaB_receptor.
R InterPro; IPR001063; FaB_receptor.
R Pfam; PR00050; TNFR_c6; 3.
R PRINTS; PR01680; PASRECEPTOR.
R SMART; SM00005; DEATH; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS50017; DEATH DOMAIN; 1.
R PROSITE; PS50050; TNFR_NGFR_1; 2.
R POMAIN 17 323 TUMOR INCERCESION SUPPORTEMENT (F. DOMAIN 17 170 Extracellular (Potential).
T TRANSMEM 17 188 POTENTIAL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Death.
By similarity.
N-linked (GlCNAc. ..) (Potential).
N-linked (GlCNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.4%; Score 233; DB 1; Length 323; 31.7%; Pred. No. 5.5e-12; Live 32; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      153 VLQECNSTANTVCSSSVSNPRN--RLFLLLSPLSVLIVSVVVFR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -linked (GlcNAc. . .) (Po 4D88A90E9E1F4892 CRC64;
                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: September 9, 2005, 09:19:10 Job time: 741.143 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36445 MW;
                                                           EMBL; U34794; AAC48546.1; -. HSSP; P25445; 1DDF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38
115 1
323 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULPID
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AC1315698 Rattus no
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AB111447 AC129123 AC103222 CR761221 BC075302 AC123379

AC128137 AC131076 AC136115 AC074039

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Best Local Similarity 100.0%; Pred. No. 8e-182;
Matches 702; Conservative 0; Mismatches 0; Indels
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9 from patent US 6627199
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Mus musculus decoy TRAIL receptor 2 long form (Dctrailr2) mRNA, Complete cds; alternatively spliced.

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        secreted soluble form; member of the TNFR family;
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Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Heutig, Y.-M., Burkly, L., Tschopp, J. and Zheng, T. S.
That Contains Two Novel Murine Receptors for Tumor Necrosis Factor Receptor Locus Factor-related Apoptosis-inducing Ligand (TRALL)
J. Biol. Chem. 278 (7), 5444-5454 (2003)
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CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
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/note="mDcTRAILR2S; binds both murine and human TRAIL;
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                                                                                                                                             TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA
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/mol_type="mRNA"
/strain="NIH Swiss"
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/chromosome="7"
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Matches 657; Conservative 0; Mismatches 0;
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Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Heuriy, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.
Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor related Apoptosis-inducing Ligand (TRAIL)
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                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S.
Direct Submission
Submitted (16-0CT-2002) Institute of Biochemistry, University of Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="mDcTRAILR2L; binds both murine and human TRAIL; membrane-bound form; member of the TNFR family; allernatively spliced" /codon_start=1
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Matches 657; Conservative
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Figure 18265 669 bp mRNA linear ROD 06-MAR-2002 Mus musculus domesticus mRNA for tumor necrosis factor receptor p60 homologue 2 (Tnfrh2 gene).
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Submitted (30-MAY-2000) Engemann S., Department Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCGAAAATTTCCA 420
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                  CAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGAT
                                 GCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAAGACGTC
                                                                                                         TGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACT
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Thfrh2 gene, tumor necrosis factor receptor p60 homolog
Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
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/mol_type="mRNA"
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SKCPAGEWRWSDVCCKNCSAGTFVKAPELBHYTGQCERCHFGTFTEKDNYLDACIL
CSTCDKOGRWYADCSATSDRKCQCRTGLYXYDPKFPESCRPCTKCPQGIPVLQBCNST
ANTVCSSSVSNPRRLFLLLSPLSPLSVLIVSVVVPRIIRF
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                                                                                                      TITCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA 480
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Risser, P., Mao, W., Baldwin, D. and Pan, G.
Characterization of SOBa, a murine member of the TNFR family
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Pred. No. 3.2e-152;
0; Mismatches 1; Indels 45;
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/product="TNF receptor family member SOBa"
/protein_id="AAL050/3.1"
/db_xref="GI:18056436"
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/bxctein.id="CAC16406.1"
/db_xref="GA1:11191812"
/db_xref="GA1:11191812"
/db_xref="GA1:09ER62"
/db_xref="GA1:09ER62"
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KCHBGTPTEKDNYLAGILCSTCDKADGENWANDCSATSDRKCQCRTGLYYYDPKFPESC
RPCTKCPQGIPVLQBCNSTANTVCSSSVSRRSASVAWPI"
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                                                                                                                                                                                                                                           82.4%; Score 578.6; DB 10; Length 669;
llarity 97.3%; Pred. No. 6.9e-148;
Conservative 0; Mismatches 12; Indels 6;
 /sub_species="domesticus"
/db_xref="taxon:10092"
/chromosome="7"
                                                                                                      /evidence=experimental
                                                 /gene="Tnfrh2"
83. .508
                                                                           gene="Tnfrh2"
                                                                                        /codon_start=1
                                                               .508
                                         .669
                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                     Matches 640;
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Best Local 9
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PAT 18-DEC-2003

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AR403757 1200 bp 1 Sequence 13 from patent US 6627199. AR403757

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Isolation, identification and characterization of tmst2, a novel member of the TNF-receptor supergene family
Patent: US 6627199-A 5 30-SEP-2003;
Location/Qualifiers
                                                                                                                                           tmst2, a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGC
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                                                                                                                                      Isolation, identification and characterization of member of the TNF *receptor supergene family Patent: US 6627199-A 13 30-SEP-2003; Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.7e-129;
Matches 511; Conservative 0; Mismatches 0;
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Sequence 5 from patent US 6627199.
AR403752.
AR403752.1 GI:40151460
                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
/mol_type="genomic DNA"
Unclassified.
1 (bases 1 to 1200)
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TGTGTGCAGTTCATCTGTTTCAA 481
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              53.8%;
        Ouery Match
Best Local Similarity 90.77
Matches 402, Conservative
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Mus musculus TNF receptor family member SOB mRNA, complete cds.
AY046550
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SNDVCCKTFCFGGTFVKAPCKLPHTQGQCEKCHFGTFTGKDNGLHDCELCSTCDKDQNM
VADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS
NPRNWLFLLMIIVFGI"
                                                                                                                                                                                                                                                            CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC 300
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                                                                                                                                                                                                                                                                                                                                                            CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. (bases I to 531)
Pan, G., Mao, W. and Risser, P.
Characterization of SOB, a member of the TNFR family
Unpublished
                                                                                                                                            1 TIGCACTCGGCCAIGTITGGCTICTICTGCAGCTIGGTGTCCCAGTCTGAGTCGCTGGTTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DNA
                                                                                                                            1 TIGCACTCGGCCATGITIGGCTTCTTCTGCAGCTTGGTCTCCAGTCTGAGTCGCTGGTTC
                                                                                                 Gaps
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Submitted (18-JUL-2001) Molecular Oncology, Genentech, Inc,
Way, South San Francisco, CA 94080, USA
Location/Qualifiers
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                                                                      Length 412;
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/protein_id="AAL05072.1"
/db_xref="G1:18056434"
                                                                                                  Indels
                                                                   Score 412; DB 6; Le
Pred. No. 4.5e-102;
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                                                          58.7%; Scc...
100.0%; Pred. No....
0; Mismatches
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           /organism="unknown"
/mol_type="genomic DNA"
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/db_xref="taxon:10090"
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                                                                                               Matches 412; Conservative
1. .412
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                                                                                  Similarity
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                                                                    Query Match
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569 bp mRNA linear ROD 06-MAR-2002
Mus musculus domesticus mRNA for tumor necrosis factor receptor p60
homologue 1 (Infrhl gene).
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                                                                                                                                                                                                                                                                                                                                                                                                           260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTGTCACCCAGGAACATTCACAGAGAAAAGATAATTACCTGGATGCTTGTATACTTTG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTCCACCTGTGATAAAGACCAGAATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 ATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCGTGCCGCCC 440
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                                                                                                                                                                                                                                                                                                                                         99 ATACTCCTTCAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 TCCCTCAGGTACATTTGTCAAGGCGCCCTGCAAAATCCCCCATACTCAAGGACAATGTGA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    441 ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC 500
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                         98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region: implications for a novel imprinting centre and extended
                                                                                                                                       GCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAATTTGCTATGCTAGAATT
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Thfrhl gene; tumor necrosis factor receptor p60 homologue 1.
Mus musculus domesticus (western European house mouse)
Mus musculus domesticus
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          DB 10; Length 531;
                                                                        Indels
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1. .569
/organism="Mus musculus domesticus"
                                                                            41;
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20519229
Score 377.4; DB 1. Pred. No. 1.5e-92; 0; Mismatches 41.
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/sub_species="domesticus"
/db_xref="taxon:10092"
/chromosome="7"
1. .569
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Lugovskoy, A.,

human TRAIL;

ORIGIN

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/gene="Dctrailr1"
/note="mDCTRAILR1; binds murine TRAIL but not human TRJ
contains a glycosyl-phosphatidylinositol (GPI) anchor;
member of the TNPR family"
Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A. Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Hsu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S. Direct Submission
Submitted (16-07-2002) Institute of Biochemistry, University Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland Location/Qualifiers
                                                                                                                                                                                                 1. .1491
/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL"
/db xref="taxon:10090"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                      /gene="Dctrailr1"
/note="Synonym: Infrh1"
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Local Similarity 90.7%;
Les 402; Conservative
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Best Local Si
Matches 402,
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Schneider, P. Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Hertig, S., Hofmann, K., Van Vlijmen, H., Heu, Y.-M., Burkly, L., Tschopp, J. and Zheng, T.S. Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL)
J. Biol. Chem. 278 (7), 5444-5454 (2003)
                                                                                                                                                                                                 /db_xref="G1:11191810"
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/db_xref="UniProc! Swiss-Prot:Q9ER63"
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RPCTKCPQGIPVLQBCNSTANTVCSSSVSNPRNWLFLLMLIVPCI"
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1491 bp mRNA linear ROD 19-FEB-2003
AY165625.1 GI:27985587
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                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 377.4; DB 10
Pred. No. 1.5e-92;
0; Mismatches 41;
                                                                                                                                            /product="tumor necrosis
/protein_id="CAC16405.1"
                                                                                                                       /evidence=experimental
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Mus musculus
  /gene="Tnfrh1"
79. .522
                                                                                            codon_start=1
                                                           gene="Tnfrh1"
                                                                                                                                                                                                                                                                                                                                                                                                                                       53.8%;
llarity 90.7%;
Conservative
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Best Local S:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
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VADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS
NPRNWLFLLMLIVFCI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG
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                                                                                                                                                                                                                                                          DB 10; Length 1491;
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                                                                                                                                                                                                                                                          Score 377.4; DB 10;
Pred. No. 1.5e-92;
0; Mismatches .41;
/product="decoy TRAIL receptor
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AR164284
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/db_xref="GI:27985588"
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ORGANISM

VERSION KEYWORDS

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FEATURES TITLE

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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 7, clone RP23-6117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baldwin, J., Barna, N., Bastien, V., Beda, F., Campopiano, A., Caslle, A., Choepel, Y., Colangelo, M., Collins, S., Colliymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 ATACTCCTTCAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TICTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGA 260
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Mus musculus chromosome 7, clone RP23-6117, complete sequence.
ACO68006
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                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6; Length 1509;
                                                                                                                                                                                               Polynucleotide encoding secretory membrane protein Patent: US 6271366-A 3 07-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      53.8%; Score 377.4; DB 6 90.7%; Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
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/organism="unknown"
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                                                                                                                            1 (bases 1 to 1509)
Kimura, N. and Toyoshima, T.
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AR164284.1 GI:16235373
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TITLE JOURNAL REFERENCE AUTHORS

REFERENCE AUTHORS

Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Anderson, M., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camarata, J., Chang, J., Chope, T., Chope, T., Colo, A., Cooke, P., Cocke, P Luserc Summassion

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Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 203141)

Birran, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,

Roderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,

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Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,

Maldrim, J., Mchous, L., Norbu, C., O'Connor, T., O'Donnell, P.,

O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,

Ramsamy, U., Ramsamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,

Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,

Spencer, B., Stange-Thomann, W., Scojanovic, N., Stubbs, M.,

Vassiliev, H., Verkataraman, V.S., Viel, R., Via, A., and Sody, M.

Direct Submission. Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Lileo, T., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Madcdonald, P., Marquis, N., McCarthy, M., McBwan, P., McGurk, A., Mirchana, K., Moheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Whrphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Spoov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Severy, P., Sponcer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Young, G., Submission Submitted (05-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 203141)

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149180 CTTATCCCCAGGTACATTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATG 149121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MWU276505 281000 bp DNA linear ROD 06-MAR-2002 AUS musculus genomic fragment, 281000 bp, chromosome 7. AJ276505
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carS gene; Cdknlc gene; cyclin-dependent kinase inhibitor 1C;
cysteinyl-tRNA-synthetase; IPL gene; Itm gene; Napll4 gene;
oysteinyl-tRNA-synthetase; IPL gene; Itm gene; Napll4 gene;
nucleosome assembly protein 1-like 4 protein; Obph1 gene; oxysterol
binding protein; Thfrhl gene; Thfrh2 gene; tumor necrosis factor
receptor p60 homologue 1; tumor necrosis factor receptor p60
homologue 2; tumor suppressing subtransferable candidate 5.
Mus musculus domesticus (western Buropean house mouse)
Mus musculus domesticus
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 CTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATG 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 TGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACT 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Engemann, S., Strodicke, M., Paulgen, M., Franck, O., Reinhardt, R., Lane, N., Reik, W. and Walter, J.
Sequence and functional comparison in the Beckwith-Wiedemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 203141;
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15618. .15787
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MMU276505
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Some of the sequence contained within base pairs 1 - 31513 was stolen from accession AC023248.

Location/Qualifiers
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DRDVPIKEESSGGTELFWTPSBEVRRQRLKRHTVLLEBQSELESERLWGHVTRAIREG
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SGSTPESCPDLSDEPVPGGESPCPRCRREYHRLKMLGEAVLSIQEAQQELHRHLSTM
LSSTVRAGQAPAPSLLQNPRSWFLLCIFLTCQLFINYILK"
                                                                                                                                                                                                             Submitted (17-MAR-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, SERMANY
Revised by autor 22-MAY-2000
3 (bases 1 to 281000)
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (22-NOV-2000) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
Berlin, GERMANY
4 (bases 1 to 281000)
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Submitted (24-JAN-2001) Engemann S., Dep. Trautner,
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195
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region: implications for a novel imprinting centre and extended
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin, GERMANY
On Jan 27, 2001 this sequence version replaced gi:11191799,
related accession numbers AJ300452-AJ300460
has a 1000 bp overlap with AJ271885.
Location/Qualifiers
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                                                                                                              1063728
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AUTHORS
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207

177

42;

Length 262; Indels

DB 6;

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181 TGTGAGAAGTGTCACCCAGGAACATTCACAGGGAAAGATAATGGCCTGCATGATGTGAA 240
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                                                                                                                          18.7%;
ilarity 75.2%;
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RPCTKCPQGIPVLQBCNSTANTVCSSSVSNPRNWLFLLMLIVFCI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                 /ocdon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATG
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PE Corporation (NY) (US)
Location/Qualifiers
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Best Local Similarity
Matches 142; Conserv
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CQ731135
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DEFINITION
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SOURCE
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

8, 2005, 15:59:37; Search time 352.87 Seconds (without alignments) 3255.208 Million cell updates/sec September Run on:

US-10-622-407-9 702 Title: Perfect score:

1 ttgcactcggccatgtttgg......ttttattgctatgaagtgat 702 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1202784 segs, 818138359 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	88 - T	SUMMARIES	g 0
-	702	100.0	702	4.	US-09-612-033B-9	ກັເ
7	602	82.8	1550	4	US-09-612-033B-7	7,
m	511	72.8	1200	4	US-09-612-033B-13	Sequence 13, Appl
4	412	58.7	412	4	US-09-612-033B-5	Sequence 5, Appli
	377.4	53.8	1509	m	US-09-411-722-3	'n
9	377.4	53.8	1509	4	US-09-855-266A-3	Sequence 3, Appli
C 7	48.8	7.0	325	7	US-08-531-927B-3	Sequence 3, Appli
ω U	47.6	6.8	1776	7	US-08-531-927B-1	Sequence 1, Appli
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Sequence 18, Appl Patent No. 5273901	Patent No. 5482/09 Patent No. 5273901	Patent No. 5482709	Sequence 10, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 5, Appli	Sequence 41, Appl	Sequence 13, Appl	Sequence 14, Appl	Sequence 5, Appli	Sequence 5, Appli	Sequence 1, Appli	Sequence 1, Appli
US-09-497-822C-18 5273901-10	5273901-10	5482709-9	US-09-521-511C-10	US-08-997-685A-1	US-09-115-446-1	US-09-565-590-1	US-09-115-446-5	US-09-565-590-5	US-08-457-273B-41	US-08-556-419-13	US-09-041-886-14	US-08-246-982A-5	US-08-453-265-5	US-09-135-994-1	US-09-684-843A-1
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ALIGNMENTS

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Sequence 9, Application US/09612033B

Sequence 9, Application US/09612033B

Sequence 10. 6627199

GENERAL INFORMATION:

JAPLICANT: Sarial, Chris

TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily

TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily

TITLE OF INVENTION: of Genes

FILE REFERENCE: 01017/35434A

CURRENT FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/143,063

PRIOR APPLICATION NUMBER: US 60/143,063

PRIOR PILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 15

SEQ ID NO 9

LENGTH: 702
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                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (13)..(552)
OTHER INFORMATION: Primer 2086-39
                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: CDS
US-09-612-033B-9
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Sequence 13, Application US/09612033B
Patent No. 6627199
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Lumit, and Characterization of
TITLE OF INVENTION: Lumit, and Characterization of
TITLE OF INVENTION:
TITLE OF INVENTION:
GENERAL TITLE OF INVENTION:
FILE REFERENCE: 01017/35434A
CURRENT APPLICATION NUMBER: US/09/612,033B
CURRENT FILING DATE: 2000-07-07
PRIOR PELICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
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                                                                                                                                            CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAAATGGTGGCCGACTGC 360
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  181 GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCC 240
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                                                               CCTTTGAGTGTGTCTAATTGTGTGTGTGTTGTTGTTCCGTATCATAAGAAGATAAAGGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: Fusion protein OTHER INFORMATION: consisting of Mus musculus sequences and OTHER INFORMATION: Immunoglobulin sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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100.0%; Pred. No. 2.2e-153;
ive 0; Mismatches 0;
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 511; Conservative
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Sequence Co. 627199
Sequence Co. 6627199
GENERAL INFORMATION:
APPLICANT: Saris, Chris
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: of Genes
CURRENT FILING DATE: 1000-07-07
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
SEO ID NO 7
                                                                             TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA 420
                                                                                                                     TCAGCCACCAGGGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA 420
                                                                                                                                                             TITCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              661 TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAGTGAT 702
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OTHER INFORMATION: mouse tmst2
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LOCATION: (13)
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US-09-612-033B-7
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US-09-612-033B-7
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                                                                                 241 CATACTCAAGGACAATGTGAGAAGTGTCACCCCAGGAACATTCACAGAGAAAGATAAATTAC 300
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                                                                CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC
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APPLICANT: Kimura, Nacki
APPLICANT: Kimura, Nacki
APPLICANT: TOYOSHima, Tomoko
TITILE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501/040001
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 12
SOFWARE: FEBLESQ for Windows Version 4.0
SEQ ID NO 3
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Pred. No. 2e-110;
0; Mismatches 41;
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US-09-411-722-3
'Sequence 3, Application US/09411722
'Patent No. 6271366
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Best Local Similarity 90.7
Matches 402; Conservative
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; LOCATION: (12)...(539)
US-09-411-722-3
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; Sequence 5, Application US/09612033B
; Patent No. 6627199;
; GENERAL INFORMATION:
    APPLICANT: Saris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: Lemst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: Of Genes
; TITLE OF INVENTION: Of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR PELING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver: 2.0
; SEQ ID NO 5
; LENGTH 412
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                                                                                                                                                                       CAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGT 312
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 CTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAATTTGCTATG 120
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                                                       CTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGC
                                                                                                                       CAATGTGAGAAGTGTCACCCAGGAACATTCACAGGAAAGATAATTACCTGGATGCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: (13)..(411)
OTHER INFORMATION: tmst2 00004-dl
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US-09-612-033B-5
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US-09-612-033B-5
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410 ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 ACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110 ATACTCCTTCAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCCATACTCAAGGACAATGTGA 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG 320
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                                                                                                                                                                                                                                                                    APPLICANT: TOYOSHIMS, Naoki
APPLICANT: TOYOSHIMS, TOMOKO
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 66501-04002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT APPLICATION NUMBER: US 09/411,722
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-40-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: 1997-04-01
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FASTESE for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 2e-110;
0; Mismatches 41
                                                                    TGTGTGCAGTTCATCTGTTTCAA 523
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US-09-855-266A-3
; Sequence 3, Application US/09855266A
----nt No. 6784284
                                         501 TGTGTGCAGTTCATCTGTTTCAA
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                                                                                      셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                   APPLICANT: Kakizuka, Akira
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
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TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph
Patent No. 5840491
TITLE OF INVENTION: Disease Gene and Uses Thereof
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48.8; DB 2; Length 325;
Pred. No. 2.5e-05;
1; Mismatches 33; Indels (
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PatentIn Release #1.0, Version #1.30
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REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUBER: ATH95-01A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION: 435
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APPLICATION DATA:
APPLICATION NUMBER: JP H6-251600
FILING DATE: 21-SEP-1994
ATTORNEY/AGENT INFORMATION:
Sequence 3, Application US/08531927B Patent No. 5840491 GENERAL INFORMATION:
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ZIP: 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
POPTION TYPE: TOWN TYPE: POPTION TYPE: 
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TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 3:
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STREET: TWO ...
CITY: Lexington
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 66.74
Matches 68; Conservative
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LENGTH: 325 base pairs
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FEATURE:
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RESULT 7

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APPLICATION NUMBER: US/09/254,590
FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-WAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
                                                                                                     NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 9-LJ 2626
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Silvia, Christopher P
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; Sequence 44, Application US/09922364A
; Patent No. 669293;
; GENERAL INFORMATION:
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ADDRESSEE: Townsend and
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%;
Best Local Similarity 66.7%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
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                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY:
; LOCATION:
US-09-041-886-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 GCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGT 119
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Patent No. 623872

GENERAL INFORMATION:
APPLICANT: Bradesen, Dale E.
APPLICANT: Rabizadeh, Sharroz

TITLE OF INVENTION: Proapoptotic Peptides, Dependence
TITLE OF INVENTION: Polypeptides and Methods of Use
NUMBER OF SEQUENCES: 72

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
3: Hamilton, Brook, Smith & Reynolds, P.C.
Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1995
CLASSIFICATION NUMBER: US/08/531,927B
FILING APPLICATION NUMBER: US/08/531,927B
FILING DATE: 21-SEP-1994
ATTONNEY/AGENT INFORMATION:
NAME: CRANATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION 10F0RMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                  STATE: Massachusetts
COUNTRY: USA
ZIP. 02173-4799
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1776 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                Lexington
Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , LOCATION: 36..1115
US-08-531-927B-1
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
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        ADDRESSEE:
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                                                                                                                                                                                                                               Gape
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Length 1776;
                                                                                                                                                                                                                     Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              972 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 931
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Score 47.6; DB 3;
Pred. No. 0.00017;
0; Mismatches 34;
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FILING DATE: 10-SEP-1997
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 62.7
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
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US-10-115-415-44/c
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Calcium-Activated Potassium Channels and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 Agricia de construció de constructo de c
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62.7%; Pred. No. 0.0002;
tive 0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: .
LOCATION: 1..2224
COTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein 3 (FSK3) full-length cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: CALLOLINGA

ZIP: 94111-3834

ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BY PETCHIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
PILING DATE: 10-Mar-1999

CLASSIFICATION NUMBER: US 60/026,451

FILING DATE: 11-SEP-1996

APPLICATION NUMBER: US 60/040,052

FILING DATE: 07-MAR-1997

APPLICATION NUMBER: US 60/045,233

FILING DATE: TARRELISE POTARRELISE POTARRELISE OF WAR-1997

APPLICATION NUMBER: US 60/045,233

FILING DATE: NUMBER: US 60/045,233

FILING DATE: NUMBER: US 60/045,233
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ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                               ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
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FILING DATE: 10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2224 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Matches 74; Conservative
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US-09-254-590-44/c
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Bond, Chris T.
Silvia, Christopher P.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "rat small conductance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                     NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calcium-activated potassium channel protein 3 (rSK3) full-length cDNA" SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thereof
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adelman, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: -
LOCATION: 1..2224
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 48
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-116-260-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE
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Mayle, James
Bond, Chris T.
Silvia, Christopher P.
TITLE OF INVENTION: Small and Intermediate Conductance,
Calcium-Activated Potassium Channels and Uses
Thereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 47.6; DB 4; Length 2224; 62.7%; Pred. No. 0.0002; Live 0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..2224
OTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein 3 (rSK3) full-length cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/116,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
             FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 31,677
TELEPHONE: (415) 576-0300
TELEFAK: (415) 576-0300
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/254,590
APPLICATION NUMBER: US/09/254,590
APPLICATION NUMBER: US 60/026,451
US 60/045,233
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ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYBER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/10116260 Patent No. 6828123 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                              LENGTH: 2224 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Adelman, John P.
                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid_
STRANDEDNESS: single
                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 48
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                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: CDNA
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
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Calcium-Activated Potassium Channels and Uses
Thereof
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                       APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
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calcium-activated potassium channel
protein 3 (rSK3) full-length cDNA"
SEQUENCE DESCRIPTION: SEQ ID NO: 44:
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
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APPLICATION NUMBER: US/10/115,671
FILING DATE: 03-Apr-2002
CLASSIFICATION: <Unknown>
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Bond, Chris T.
Silvia, Christopher P.
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TELEFAX: (415) 576-0300
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                                                                                                                         FILING DATE: 07-MAR-1997
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ADDRESSEE: Townsend and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 44: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.8%; Score 47.6; DB 4; Length 2224; ilarity 62.7%; Pred. No. 0.0002; Conservative 0; Mismatches 44; Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "rat small conductance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,364A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                    NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REPERENCE TOWNER: 31,677
REPERENCE TOWNER: 014210-000730US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFARA: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
                   FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
FILING DATE: 17-AR-1997
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium-accivatow: /note= "rat sma calcium-accivated potessium channel protein 3 (rSK3) full-length cDNA"; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
APPLICATION NUMBER: US/09/254,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Adelman, John P.
Maylie, James
Bod, Chris T.
Silvia, Christopher P.
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US-09-922-364A-48/c
Sequence 48, Application US/09922364A
Patent No. 6692937
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1..2224
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: -
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1es 74; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.8%; Score 47.6; DB 4; Length 2462; Best Local Similarity 62.7%; Pred. No. 0.00021; Matches 74; Conservative 0; Mismatches 44; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION:
                                                                                                                                                                                                                                                    FILING DATE: 10-Mar-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 07-MAR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 17-APR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  APPLICATION NUMBER: US/09/254,590
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHRACTERISTICS:
LENGTH: 2462 base pairs
                                                                        CLASSIFICATION: <Unknown>
FILING DATE: 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                  Copyright
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- nucleic search, using sw model nucleic

8, 2005, 12:35:36; Search time 1032.11 Seconds (without alignments) 4026.354 Million cell updates/sec September

Run on:

US-10-622-407-9 702

score: Perfect

1 ttgcactcggccatgtttgg......ttttattgctatgaagtgat 702 Sequence:

IDENTITY NUC Gapox 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum

DB seq length: 0 DB seq length: 200000000 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* geneseqn1980s:* Database

geneseqn19908:* geneseqn20008:* geneseqn2001as:* geneseqn2001as:* geneseqn2002as:* geneseqn2003as:* geneseqn2003as:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004bs:*

Description	Aad64755 Mouse tms Ad364754 Mouse tms Ad364751 Mouse tms Ad364758 Mouse tms Ad364757 Murine tm Aad64758 Mouse tms Ad345757 Murine tm Ad464757 Murine tm Ad46754 Murine tm Ad56964 Novel mur Adf5750 Mouse ynk Aav68046 Nucleic a Adm46622 Mouse ynk Aav68046 Nucleic a Adm46622 Mouse ynk Aav833513 Mouse mit Ad57563 Mouse mit Ad57563 Mouse mit Ad57563 Mouse spl Abn8934 Murine TA Abn8934 Murine TA Abn89358 Mouse spl Abn89336 Murine TA
SUMMARIES	AAD64755 AD745753 AD745751 AD64751 AD64757 AD64753 AD64753 AD64753 AD75750 AD75750 AD75750 AD75750 AD75750 AD75750 ABS95750 ABS95750 ABS9334 ABS9334 ABS5525 ABS9334 ABS5525 ABS9334 ABS5525 ABS9334 ABS7550
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Acc68996 Human neu Aas87787 DNA encod	Acc68997 Human neu			Aav35473 Human hSK	Acf03947 Human SK-	0		Abk10239 Trinucleo	Abl41663 Nucleotid	Acd94759 Human col	Abl22295 Drosophil	Abl22294 Drosophil	Abl15249 Drosophil	Abl15248 Drosophil	Abd32846 Mouse can	Aaf84342 Human and	Adj92835 Human co-	Abv94246 Breast ca	Adf56532 Fusion pr	Adk67041 Gene #131	Adp22722 Human SMA	Abl66686 Lung canc	Abk84651 Human cDN
ACC68996 AAS87787	ACC68997	AAZ23425	AAV35472	AAV35473	ACF03947) ADE31740	AAS79773	ABK10239	ABL41663) ACD94759	ABL22295	ABL22294	ABL15249	ABL15248	3 ABD32846	AAF84342	2 ADJ92835	ABV94246) ADF56532	0 ADK67041	2 ADP22722	ABL66686	ABK84651
1269 10 1379 5	1423 10	1776 2	2224 2	2462 2	3095 9	3095 10	1016 5	277 3	504 4	365 10	1080 4	5264 4	5824 4	11743 4	89873 13	1810 4	4719 12	_	5257 1(5257 10	5830 13	5959 6	5959 6
8.8 .9	6.8	8.9	6.8	8.9	6.8	6.8	6.7	6.7	6.7	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9	9.9
47.6	47.6	47.6	47.6	47.6	47.6	47.6	47.2	47	46.8	46.6	46.4	46.4	46.4	46.4	46.4	46.2	46.2	46.2	46.2	46.2	46.2	46.2	46.2
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ALIGNMENTS

AAD64755 standard; cDNA; 702 RESULT 1

BP.

(first entry) 11-MAR-2004 AAD64755;

Mouse tmst2-receptor splice variant cDNA.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse; splice variant; gene; ss.

Mus musculus.

13. 555 /*tag= a /product= "Mouse tmst2 receptor splice variant protein" Location/Qualifiers Key

07-JUL-2000; 2000US-00612033. US6627199-B1. 30-SEP-2003

(AMGE-) AMGEN INC.

99US-0143063P.

09-JUL-1999;

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Saris C;

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WPI; 2003-874309/81. P-PSDB; ABW02716.

New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping.

(first entry)

06-MAY-2004

ADJ45753;

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                                              and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor splice variant cDNA used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                       CITTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCCTTGCAGGTA 120
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                                   invention relates to transmembrane decoy-receptor (tmst2) proteins
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100.0%; Pred. No. 4.6e-192;
ive 0; Mismatches 0;
NO 9; Opp; English
                                                                                                                                                                                                                   exemplification of the invention
                                                                                                                                                                                                                                                                                                         al Similarity 100. 702; Conservative
 Claim 1; SEQ ID
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ADJ45753 standard; cDNA; 702 BP.

RESULT 2 ADJ45753 ID ADJ4 XX

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, and conditions including acquired immunodeficiency syndrome (AIDS), ansemia, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents condition a murine tmst2-receptor splice
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                                                                AIDS, anaemia; autoimmune disease; autoimmune autoimmune disease; diabetes mallitus, disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphona; meningitis; multiple sclerosis; isohaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease; tmst2-receptor splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Murine tmst2-receptor splice variant"
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                                                     ss; acquired immunodeficiency
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4.6e-192;
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0; Mismatches
Murine tmst2-receptor splice variant cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 9; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

Best Local Similarity 100.0%;
Matches 702; Conservative 0
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                                                       tmst2-receptor; gene;
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The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, acachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor CDNA used in the exemplification of the invention
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Pred. No. 4.9e-163;
0; Mismatches 0;
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Best Local Similarity 93.6%;
Matches 657; Conservative
P-PSDB; ABW02715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a tmst2-receptor polypeptides and the polynuclectide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), ansemia, autoimmune diseases, cachaxia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, hademorrhagic shock, hepatitis, insulin resistance, leprosy, lenksemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents cDNA encoding the murine tmst2-receptor
                                                                                                                                                                       Mouse; tmst2-receptor; gene; ss; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
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"Murine tmst2-receptor"
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Pred. No. 4.9e-163;
0; Mismatches 0;
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93.6%;
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                                                                                                                                                 Murine tmst2-receptor cDNA
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TIGCACTCGGCCATGITIGGCTICITCTGCAGCTIGGTGTCCAGTCTGAGTCGCTGGTTC 60

TIGENTIALITY TO CONTROLL THE CON

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Matches 657; Conservative

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                                                                                                                                                                                                                                                                                                 241 CATACTCAAGGACAATGTGAGAAGTGTCACCCAAGGAACATTCACAGAAGAAGATAATTAC 300
                                                                                                                                                                                                                                                                                                                                               CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
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                                                                                                                                                                                                                                                                                                                                                                                             301 CTGGAIGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCCAAAA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAGAAGATCTGCCTCAGTG 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 GCCTGGCCTATCTGAATGGTTCACAGAGATCCCAGAAACCGGCTGTTCCTACTGTTATCA
                                                                 121 AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
                                                                                                  AAATTIGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
                                                                                                                                                          GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCCTGCGAAATCCCC
                                                                                                                                                                                       GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTCCAGAATCGTGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ATCCCAGAAACCGGCTGTTCCTACTGTTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCTTTGAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCTTTGAGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGGATAAAGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAA--------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse tmst2-receptor-human immunoglobulin Fc region chimeric DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Mus musculus.
- Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and their secreted splice variants, belonging to the tumour necrosis factor (TNP) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is a chimeric DNA comprising mouse timst2- receptor DNA and human immunoglobulin Fc region DNA. This sequence is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGT 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCG 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crecrecrecrecrecrecrecrecrecrearcreccrrrccaegraaarrrecrare 120
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                                                                                                                                                                                                                                                                                                                                                                          tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, ating or ameliorating diseases associated with or resulting from ormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to transmembrane decoy-receptor (tmst2) proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1200 BP; 293 A; 361 C; 299 G; 247 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ATGITIGGCTICTICIGCAGCTIGGTGTCCAGICTGAGTCGCTGGTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 511; DB 10; L
Pred. No. 8.3e-137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              493 GCTAACACTGTGTGCAGTTCATCTGTTTCAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SEQ ID NO 13; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exemplification of the invention
                                                         07-JUL-2000; 2000US-00612033
                                                                                                               99US-0143063P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 511; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              treating or ameliorating
                                                                                                                                                                                                                                                                                        WPI; 2003-874309/81.
P-PSDB; ABW02717.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome mapping
                                                                                                                                                                      (AMGE-) AMGEN INC
                                                                                                               09-JUL-1999;
30-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 (
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The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), ansemia, autoimmune diseases, cachexia, cancer, crebral malaria, diabetes mellitus, disseminated intravascular coagulation, halamorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obseity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents cDNA encoding a murine tmst2-Fc fusion protein of the invention.
                                                                                                                                                                                                                                 Mouse; tmst2-receptor; gene; ss; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ATGITIGGCTICTICIACAGCTIGGIGICCAGICTGAGICGCTIGGTICCTITIGGCGGCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1200 BP; 293 A; 361 C; 299 G; 247 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Murine tmst2-Fc fusion protein"
481 GCTAACACTGTGTGCAGTTCATCTGTTTCAA 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; SEQ ID NO 13; 57pp; English.
                                                                                                                                                                                                       Murine tmst2-Fc fusion protein cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                    ВР
                                                                                                    ADJ45757 standard; cDNA; 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999; 99US-0143063P. 07-JUL-2000; 2000US-00612033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-2003; 2003US-00622407
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                                                                                                                                                                                                                                                                                                                                                           tmst2-Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                          musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                     ADJ45757;
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                                                                                                   AAGAACTGTTCTGCAGGTACATTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGA 240
                                                                                                                                      CAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAAGATAATTACCTGGATGTTGT 300
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                                                                                                                                                                ATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGT 372
                                                                                                                                                                                                   GACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCG 432
                                                                                                                                                                                                                                       TGCCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCCAGGAATGCAACTCCACA 492
                                                                                                                                                                                                                                                                                                                                                                                                                        cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
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                                                                                                                                                                                                                                                                                                                                                                                                                 tmst2; tumour necrosis factor; TNF; sepsis;
ATGTTTGGCTTCTTCTGCAGCTTGGTGTCCAGTCTGAGTCGCTGGTTCCTTTGGCGGCGG
                                                                                        AAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Mouse tmst2 receptor protein"
                                                                                                                                                                                                                                                                                                                                                                                               Mouse tmst2-receptor cDNA from tmst2-00004-d1 clone.
                                                                                                                                                                                                                                                                           GCTAACACTGTGTGCAGTTCATCTGTTTCAA 523
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                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane decoy-receptor;
                                                                                                                                                                                                                                                                                                                                         AAD64753 standard; cDNA; 412
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The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TMP) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or amaliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parastic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor cDNA used in the exemplification
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2 nucleic acid molecule and polypeptide, useful for diagnosing, or ameliorating diseases associated with or resulting from tmst2 expression, e.g. sepsis, inflammation or cancer, or for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 412 BP; 93 A; 104 C; 102 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                 English
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                                                                                                                                                                                                 Example 1; SEQ ID NO 5; Opp;
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Best Local Similarity 100.0
Matches 412; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), ansemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, pymphoma, meningitis, multiple sclerosis, ischaemia, obseity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases.
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adult respiratory distress syndrome; ARDS; tuberculosis; viral disease.
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a tmst2-receptor polypeptides and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 412 BP; 93 A; 104 C; 102 G; 113 T; 0 U; 0 Other;
                                                                                            '*tag= a
'product= "Murine tmst2 00004-d1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 412; DB 12;
Pred. No. 2e-108;
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100.0%; Pred. No. 2-
'... 0; Mismatches
                                                                                                                           /partial
/note= "No stop codon shown"
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                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                    09-JUL-1999; 99US-0143063P, 07-JUL-2000; 2000US-00612033.
                                                                                                                                                                                                                                      17-JUL-2003; 2003US-00622407
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                    (SARI/) SARIS'C.
                                                                                                                                                                        JS2004018544-A1
                                Mus musculus
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The invention describes an isolated murine polynucleotide (I) comprising a contiguous stretch of at least 60 nucleotides of one of 265-677 nucleotide 891 OWNIBANK gene trapped sequences (GTSS) (S), given in the specification. The novel genes and cells are useful in functional genomic analysis and in the discovery and development of new therapeutic and disposeric agents and methods. (I) is useful for identifying the coding regions of the murine genome, to isolate cDNAs, genomic clones, or full-length genes/polynucleotides or homologues, heterologues, paralogues, or trhologues that are capable of hybridishing to one or more of the GTSs under stringent conditions. (I) can be incorporated into a phage display system that can be used to screen for proteins, or other ligands, that system that can be used to screen for proteins, or other ligands, that system that can be used to screen for proteins, or other ligands, that can expand an amino acid sequence encoded by an oligonucleotide or polynucleotide sequence in at least one of the TS sequences. (I) is useful in addressable arrays, such as gene chips, to identify and characterise temporal and tissue specific gene expression, to identify the gene of interest from many sources and for genetic manipulations such as antisense inhibition and gene targeting. Decreasing the leaf of the level of expression of (I) and/or down regulating the activity of conting the
301 CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel murine polynucleotides that individually identify novel genes into which a retroviral gene trap vector has integrated, useful in genomic analysis and in discovery, development of therapeutic and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptides or proteins encoded by (I) is useful for treating development and cell differentiation disorders, aging, cancer, autonimune disease, lupus, inflammatory disorders, skin disorders and degenerative disorders. This sequence represents a murine cDNA isolated using gene trap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; gene trapped sequence; GTS; functional genomic analysis; phage display system; gene chip; temporal gene expression; tissue specific gene expression; antisense inhibition; gene targeting; development disorder; cell differentiation disorder; aging; cancer; autoimmune disease; lupus; inflammatory disorder; skin disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel murine polynucleotide isolated using gene trap technology #737.
                                                        361 TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATG
                                                                                           361 TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATG
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                                                                                                                                                                                                                                                           ABS69674 standard; DNA; 415
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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(ZAMB/) ZAMBROWICZ B.
(SAND/) SANDS A T.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                          CTGGATGCTTGTATACTTTGCTCCACCTGTAAAGATCAGGAAATGGTGGCCGACTGC 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; cancer; acquired immune deficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                        69
                                                                                                                  121 AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA
                                                                                                                                        GACGICIGITGCAAGAACTGTICTGCAGGTACATTIGICAAGGCGCCCTGCGAAATCCCC
                                                                                                                                                                                                                                                                                                               130 CATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTAC
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                                        Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAGAA 526
BP; 119 A; 107 C; 88 G; 101 T; 0 U; 0 Other;
                                                                             Indels
                                    55.9%; Score 392.4; DB 6; 99.5%; Pred. No. 9e-103; ive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADF57550 standard; cDNA; 967 BP
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/product= '
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                                                                             Conservative
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P-PSDB; ADF57551.
                                                      Similarity
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  Sequence 415
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                                    Query Match
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The invention relates to transmembrane decoy receptor, ymkz5 belonging to tumour necrosis factor (TNF) receptor supergene family and nucleic acid sequences encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTCCACCTGTGATAAAGACCAGAATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAA 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 ATGCGAGTGCCAAATAGGTCTTTACTACTATGACCCAAAATTTCCGGAATCATGCCGCCC 401
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Novel ymkz5-receptor polypeptide useful for treating diseases such ar
tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,
leukemia, hepatitis, multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 377.4; DB 1;
Pred. No. 2.8e-98;
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                                                                                                                                        SEQ ID NO 7; 57pp; English.
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90.7%;
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Mus musculus.
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                                                                       RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes a protein designated 7F4. This protein is capable of inducing differentiation in osteoblast calls. The protein may be used to screen compounds for the ability to bind to it, for use as ligands, agonists or antagonists and inhibiting or otherwise altering its differentiation inducing activity. Compounds so identified, as well as the protein itself, DNA encoding it, and antibodies to it, may be used in the treatment of diseases of bone growth and osteoblast differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140
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for screening
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Pred. No. 3.4e-98;
0; Mismatches 41
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lular region only and can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treatment of bone growth disorders.
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                                                  sig_peptide
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The present invention relates to a transgenic non-human animal having the expression of 7F4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agents for the prevention and treatment of diseases including osteoporosis, obesity and diabetes. The present sequence represents the modified mouse 7F4 encoding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                           7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 377.4; DB 12; Length 1509;
Pred. No. 3.4e-98;
0; Mismatches 41; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expression of 7F4 ger
metabolism disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic non-human animal with modified screening remedies for bone or glycolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; SEQ ID NO 1; 44pp; Japanese
492
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TGTGTGCAGTTCATCTGTTTCAA
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90.7%;
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                                                                                                                                                    ADM46622 standard; DNA; 1509
                                                                                                                                                                                                                                                                                                                               Mouse 7F4 encoding sequence
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/product='
                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity
Matches 402; Conserv
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The invention relates to a novel array comprising at least two isolated nucleotide molecules, each molecule having a sequence capable of uniquely hybridising to a nucleotide molecule which is an expression product of a gene involved in mitochondrial blology. The array comprises two or more isolated nucleic acid molecules or spots, each molecule having a sequence chosen from sequence of 994 human probes and 2046 mouse probes. An array of the invention is useful for determining an expression profile of a mouse or human sample containing nucleic acid, by contacting the array with the sample under conditions allowing selective hybridisation, and measuring hybridisation of nucleic acid in the sample to the array to produce an expression profile. The array is also useful for determining capacity to a second, differently labelled sample containing nucleic acid. The second sample is a reference or a standard. An array is useful for ender mining an expression profile diagnostic of an energy metabolism. The acted physiological condition. An array of the invention is useful for determining mitochondrial biology gene expression profiles of organisms, such as human, mice and closely related species; tissue and organs of such organisms, which are useful for determining expression profiles of such organisms, which are useful for determining expression profiles tissue and organs of such organisms, which are useful for determining expression profiles.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Array containing probes for genes involved in mitochondrial biology, useful for determining mitochondrial biology gene expression profiles for use in diagnosing pathologies and identifying biochemical pathways.
  CTCCACCTGTGATAAAGACCAGAATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAA 349
                                                                                                                                                          ATGTACCAAGTGTCCCCAAGGAATCCCTCTCCTCCAGGAATGCAACTCCACAGGTAACAC 469
                                         ATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCGTGCCGCCC
                                                                                   ATGCGAGTGCCAAATAGGTCTTTACTACTATGACCCAAAATTTCCGGAATCATGCCGCCC
                                                                                                                                   ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; mouse; array; mitochondrial; hybridisation; energy-metabolism; mitochondrial disease; oxidative phosphorylation dysfunction; oxidative stress; apoptosis; aging.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse mitochondrial DNA sequence SEQ ID NO:1286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Procaccio V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; SEQ ID NO 1286; 201pp; English
                                                                                                                                                                                                                      TGTGTGCAGTTCATCTGTTTCAA 523
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31-AUG-2001;
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pathways, genes, and mutations involved in such physiological conditions, identifying therapeutic agents useful for preventing and/or treating such physiological conditions, evaluating and/or monitoring the efficacy of published conditions, and creating and identifying animal models of human energy metabolism-related physiological conditions. An array is also useful for defining expression signatures or profiles for mitochondrial diseases, as well as distinguishing clinical disorders that result from oxidative phosphorylation (OxHOS) dysfunction, oxidative stress, apoptosis and aging. An array of the invention contains probes of genes not previously recognised to participate in mitochondrial biology. The elemences shown in ADD33224-ADD32260 represent murine mitochondrial DNA clones used to make the probes of the invention. Some sequences are not present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour cancer; acquired immune deficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CTCCACTGTGATAAAGACCAGAATATGGTGGCTGACTGTTCTGCCACCAGTGACGGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAATTTGCTATGCTAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTCCTCTTGCTGCTGCTGCTGAATCTGTTCTTGCCGGTAATATTTGCTATGCCTGAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 ATACTCCTACAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTTGTTGCAAGACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 TCCCTCAGGTACATTTGTCAAGGCGCCCTGCAAAATCCCCCCATACTCAAGGACAATGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAGTGTCACCCAGGAACATTCACAGGGAAAGATAATGGCCTGCATGATTGTGAACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  441 ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 ACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         381 ATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCGTGCCGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCCATACTCAAGGACAATGTGA
diagnosing such physiological conditions, identifying biochemical
                                                                                                                                                                                                                                                                                                                                    53.5%; Score 375.8; DB 10; Length 603; ilarity 90.5%; Pred. No. 6.6e-98; Conservative 0; Mismatches 42; Indels 0;
                                                                                                                                                                                                                                                                                                   Sequence 603 BP; 154 A; 153 C; 127 G; 169 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse ymkz5 receptor cDNA clone ymkz5-00013-g11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTGTGCAGTTCATCTGTTTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADF57563 standard; cDNA; 357
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                                                                                                                                                                                                                                                                                                                                                         Similarity
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1906, 2408 and
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Matches
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AAS73531 standard; cDNA; 1197 BP.

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The invention relates to transmembrane decoy receptor, ymkz5 belonging to tumour necrosis factor (TMT) receptor supergene family and nucleic acid sequences encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (ADS), anaemia, autoimmune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAAAAATTTGCTATGCTAGAATT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCCTCTTGCTGCTGCTGCTGAATCTGTTTCTTGCCGGTAATATTTTGCTATGCTGAATC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATACTCCTTCAACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTTGCAAGACCTG 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rccercadgracarrigicaaddccecerdcaaaarccecearacreaadacaarargra 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTG 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAA 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTGTCACCCAGGAACATTCACAGGGAAAGATAATGGCCTGCATGATTGTGAACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                 Novel ymkz5-receptor polypeptide useful for treating diseases such as tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.1%; Score 253.2; DB 12; Length 357; 87.9%; Pred. No. 1.3e-62; Live 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 357 BP; 88 A; 94 C; 80 G; 95 T; 0 U; 0 Other;
                                           /*tag= a
/product= "Murine ymkz5 receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present sequence is mouse ymkz5 receptor cDNA.
                                                                           /partial
/note= "No stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 5; 57pp; English
Location/Qualifiers
5. .356
                                                                                                                                                                                             11-JUL-2002; 2002US-00193616.
                                                                                                                                                                                                                           09-JUL-1999; 99US-0143137P.
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Conservative
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                                        *tag=
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Les 276; Conserv
                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ADF57549
                                                                                                                                                                                                                                                                             (ZHAN/) ZHANG K.
                                                                                                                           US2003096355-A1
                                                                                                                                                            22-MAY-2003
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                                                                                                                                                                                                                                                                                                                Zhang K;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed cativity of (II) so useful for generating antibodies sequence transporting (II). (II) is useful for generating antibodies sequence involving (II). (II) is useful for generating antibodies sequent in, detecting or quantitating a useful for generating antibodies sequent are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics for produce other types of data and products dependent on DNA and aming a consequence the consequence of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357 TAAAGACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 GGTAAAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1197 BP; 289 A; 306 C; 317 G; 285 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                          DNA encoding novel human diagnostic protein #9335.
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Pred. No. 2.6e-53;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 9335; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.6%;
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                                                                                                       (first entry
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Hes 223; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG09344
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                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                       13-FEB-2002
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Search completed: September 8, 2005, 17:05:23 Job time : 1034.11 secs

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11. (cgn2_6/ptodata1//pubpna/US07_PUBCOMB.seq:*

12. (cgn2_6/ptodata1//pubpna/US07_NEW_PUB.seq:*

12. (cgn2_6/ptodata1//pubpna/US06_PUBCOMB.seq:*

13. (cgn2_6/ptodata1//pubpna/US06_PUBCOMB.seq:*

14. (cgn2_6/ptodata1//pubpna/US07_NEW_PUB.seq:*

15. (cgn2_6/ptodata1//pubpna/US08_NEW_PUB.seq:*

15. (cgn2_6/ptodata1//pubpna/US08_PUBCOMB.seq:*

16. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

17. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

18. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

19. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

10. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

11. (cgn2_6/ptodata1//pubpna/US09_PUBCOMB.seq:*

12. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

13. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

14. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

15. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

16. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

17. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

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11. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

12. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

13. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

14. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

15. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

16. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

17. (cgn2_6/ptodata1//pubpna/US10_PUBCOMB.seq:*

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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 9, Appli	Sequence 7, Appli	Sequence 13, Appl	Sequence 5, Appli	Sequence 737, App	Sequence 737, App	Sequence 7, Appli
2111111	ΩI	7 US-10-622-407-9	US-10-622-407-7	US-10-622-407-13	US-10-622-407-5	US-09-728-445-737	US-10-964-549-737	US-10-193-616-7
	8	17	11	17	17	6	22	14
	* Query Match Length DB ID	702	1550	1200	412	415	415	196
	Query Match	100.0	85.8	72.8	58.7	55.9	55.9	53.8
	Score	702	602	511	412	392.4	392.4	377.4
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Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 28273, A Sequence 11546, A Sequence 43, Appl	* 4 4 4 4 4 4 4 0 0 0 0 0 0 0 0 0 0 0 0	Sequence 26238, A Sequence 103, App Sequence 475, App Sequence 475, App Sequence 26, Appl
9 US-09-855-266A-3 19 US-10-802-332-3 10 US-01-193-615-5 14 US-10-198-846-11546 14 US-10-198-846-11546 20 US-10-489-372-43	9 US-09-284-344 13 US-10-115-695-44 14 US-10-115-695-44 14 US-10-115-61-44 14 US-10-115-61-44 15 US-10-115-61-44 16 US-10-115-61-44 17 US-10-278-698-74 18 US-10-278-698-74 19 US-09-282-364A-48 19 US-09-282-364A-48 10 US-10-115-695-48 11 US-10-115-69-48 12 US-10-115-69-48 13 US-10-115-61-48 14 US-10-115-61-48 15 US-10-115-61-48 16 US-10-115-61-48 17 US-10-115-61-48 18 US-10-115-61-48 19 US-10-115-61-48 10 US-10-115-61-48 11 US-10-115-61-48 12 US-10-115-61-48 13 US-10-115-61-48 14 US-10-115-61-48 15 US-10-115-61-48 17 US-10-115-61-48 18 US-10-956-157-995 21 US-10-956-157-995 21 US-10-956-157-4070 10 US-10-956-157-4070 10 US-10-956-157-4070 10 US-10-954-456-1996	18 US-10-425-114-26238 20 US-10-737-450-103 15 US-10-037-270-475 17 US-10-117-722-475 19 US-10-618-941-26
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ALIGNMENTS

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RESULT 1

1. Sequence 9, Application US/10622407

1. Sequence 9, Application US/10622407

2. Dublication No. US20040018544A1

3. GENERAL INFORMATION:

4. APPLICANT: Saris, Chris

5. TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

7. TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

7. TITLE OF INVENTION: MEMBER: US/10/622,407

7. TITLE OF INVENTION: MEMBER: US/10/622,407

7. CURRENT APPLICATION NUMBER: US/012,033

PRIOR PELLING DATE: 2000-07-07

PRIOR PELLING DATE: 1999-07-09

8. PRIOR FILING DATE: 1999-07-09

8. NUMBER OF SEQ ID NOS: 15

8. SOFTWARE: Patentin Ver. 2.0

8. SEQ ID NO 9

1. LENGTH: 702

1. LENGTH: 702

1. TYPE: DNA

9. ORGANISM: Mus musculus

1. FEATURE:

1. CCATION: (13)..(552)

1. PRATURE:

1. OTHER INFORMATION: Primer 2086-39

10S-10-622-407-9
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APPLICANT: SALIS, Chris
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOT
TITLE OF INVENTION: MEMBERS OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
TITLE OF INVENTION: MEMBERS OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
TILE REFERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2003-07-17
PRIOR PELICATION NUMBER: US 09/612,033
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 2000-07-07
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Pred. No. 4.4e-179;
0; Mismatches 0;
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                    ; IOCATION: (13)..(606)
; FEATURE:
; OTHER INFORMATION: mouse tmst2
US-10-622-407-7
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93.6%;
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   NAME/KEY: CDS
LOCATION: (13)..(606)
FEATURE:
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TITLE OF INVENTION: IDSUATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
TITLE OF INVENTION: MEMBER OF THE THF-RECEPTOR SUPERFAMILY OF GENES
FILE REPERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT APPLICATION NUMBER: US/09/612,033
PRIOR FILING DATE: 2003-07-17
PRIOR FILING DATE: 2000-07-07
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PACENTIN VET: 2.0
SOFTWARE: PACENTIN VET: 2.0
SEQ ID NOS: 15
SOFTWARE: PACENTIN VET: 2.0
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 Mismatches
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 702; Conservative
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ORGANISM: Mus musculus
FEATURE:
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APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020102543Alel Mutated Mammalian Cells and
TITLE OF INVENTION: Animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATG 412
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Pred. No. 4.1e-113;
0; Mismatches 1;
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CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 737, Application US/09728445; Patent No. US20020102543A1; GENERAL INFORMATION:
                                                                                                                                                                                                                             OTHER INFORMATION: tmst2 00004-d1
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 412
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                                                                                               ORGANISM: MUB MUBCULUB
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(411)
FEATURE:
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; ORGANISM: Mus musculus
US-09-728-445-737
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/622,407

PRIOR PRILOK APPLICATION NUMBER: US 09/612,033

PRIOR PILING DATE: 2000-07-07

PRIOR PILING DATE: 1999-07-09

NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Fusion protein OTHER INFORMATION: consisting of Mus musculus sequences and OTHER INFORMATION: Immunoglobulin sequences
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1200;
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Publication No. US20040018544A1
GENERAL INFORMATION:
                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
  PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                         ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1194)
US-10-622-407-13
                                                                                                      LENGTH: 1200
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US-10-622-407-5
                                                                               SEQ ID NO 13
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TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: ymkz5, a novel
TITLE OF INVENTION: ymkz5, a novel
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
FILE REFERENCE: 01017/35551A
CURRENT APPLICATION NUMBER: US/10/193,616
CURRENT FILING DATE: 2002-07-11
PRIOR PLLING DATE: 2000-07-07
PRIOR PLLING DATE: 1999-07-07
PRIOR PLLING DATE: 1999-07-07
NUMBER: US 60/143,137
PRIOR FILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 3.5e-108;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10193616; Publication No. US20030096355A1; GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 402; Conservative C
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NAME/KEY: CDS
LOCATION: (4)..(531)
OTHER INFORMATION: Mu-ymkz5
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US-10-193-616-7
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GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCC
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals
TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals
FILE REPERENCE: LEX-028-UGA
CURRENT FILING DATE: 2004-10-13
CURRENT FILING DATE: 2000-12-28
PRIOR PILING DATE: 2000-12-28
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 4.1e-113;
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99.5%; Pred. No. 4...
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ORGANISM: Mus musculus
US-10-964-549-737
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; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
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Pred. No. 4.4e-108;
0; Mismatches 41; Indels 0;
Sequence 3, Application US/10802332
Publication No. US20040152879A1
GENERAL INFORMATION:
APPLICANT: Kimura, Nacki
APPLICANT: Troyoshima, Tomcko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/10/802,332
CURRENT PILING DATE: 2004-03-16
PRIOR PILING DATE: 2001-05-14
PRIOR PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 9/411,722
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: US 9/099653
PRIOR FILING DATE: 1997-04-01
PRIOR SPELING DATE: 1997-04-01
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US-10-802-332-3
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APPLICANT: TOYOSHIMA, TOMOKİ

APPLICANT: TOYOSHIMA, TOMOKİ

TITLE GEN ENVENITON: NOVEL SECRETORY MEMBRANE PROTEIN

FILER REFERRANCE: 06501-040002

CURRENT APPLICATION NUMBER: US/09/855,266A

CURRENT PILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1997-04-01

PRIOR FILING DATE: 1997-04-01

PRIOR FILING DATE: 1997-04-01

NUMBER: OF SEQ ID NOS: 13

SOPTWARE: FASESEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 1509
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                                                                                                                   TGTGTGCAGTTCATCTGTTTCAA 484
                                                                                                                                                                                                                                                                                                                                                         ; Sequence 3, Application US/09855266A; Patent No. US20020128435A1; GENERAL INFORMATION:
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Matches 402; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: (12)...(539)
US-09-855-266A-3
                                                                                                                                                                                                                                                                                                                      US-09-855-266A-3
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US-10-802-332-3
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APPLICANT: Lillie, James
APPLICANT: Allie, James
APPLICANT: Allie, James
APPLICANT: As Statemenn, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION WINDER: US/10/198,846
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT PILING DATE: 2002-07-18
PRIOR FILLING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11546
                                                                                                                                              567 AGATCCCAGAAACCGGCTGTTCCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 GCTTCTTCTGCAGCTTGGTGTCCAGTCTGAGTCGCTGGTTCCTTTGGCGGCGGCTGCTGC
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                                                 Score 60.2; DB 10; Length 65;
Pred. No. 1.7e-08;
0; Mismatches 3; Indels (
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Pred. No. 0.00078;
0; Mismatches 51;
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; Publication No. US20030099974A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: INCYTE GENOMICS, INC.
APPLICANT: HONCHELL, Cynthia D.
APPLICANT: WARREN, Bridget A.
APPLICANT: BOROWSKY, MAYK L.
APPLICANT: GRIFFIN, Jennifer A.
APPLICANT: LI, Joana X.
APPLICANT: LIS, SOO YEUN
APPLICANT: LEE, SOO YEUN
APPLICANT: LEE, SOO YEUN
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                                                      8.6%;
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Best Local Similarity 60.8%;
Matches 79; Conservative
                                                 Query Match
Best Local Similarity 95.4°
Matches 62; Conservative
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US-10-198-846-11546/c
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           US-09-908-975-28273
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APPLICANT:
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APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: WASSERMAN, Alon
APPLICANT: WINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLECTINE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
FILE REPERENCE: 3668-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR PRILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PATENTIN VERSION 3.0
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TITLE OF INVENTION: member of the TNF-Receptor Supergene Family FILE REFERENCE: 01017/35551A
CURRENT APPLICATION NUMBER: US/10/193,616
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US/09/611,989
PRIOR FILING DATE: 2000-07-07
PRIOR PELLING DATE: 1090-07-07
PRIOR PILING DATE: 1999-07-07
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 5.
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Pred. No. 3.9e-69;
0; Mismatches 38; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 87.9%;
Matches 276; Conservative
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LENGTH: 65
TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                      ORGANISM: Mus musculus
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; LOCATION: (6)..(356)
US-10-193-616-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: JIN, Pei
APPLICANT: LEE, Sally
TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
FILE REPERENCE: PF-1185 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.8%; Score 47.6; DB 20;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 68; Conservative 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7505821CB1
US-10-489-372-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2004-03-12.
PRIOR PELING DATE: 2001-09-14
PRIOR PELING DATE: 2001-09-14
PRIOR PELING DATE: 2001-09-18
PRIOR PELING DATE: 2001-09-28
PRIOR PELING DATE: 2001-00-04
PRIOR PELING DATE: 2001-00-04
PRIOR PELING DATE: 2001-10-04
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-11-02
PRIOR PELING DATE: 2001-11-02
PRIOR PELING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR PELING DATE: 2001-11-07
PRIOR PELING DATE: 2001-10-07
PRIOR PELING DATE: 2001-10-07
PRIOR PELING DATE: 2001-10-07
PRIOR PELING DATE: 2002-01-04
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PRIOR PELING DATE: 2002-01-04
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                                                                                                                                                                                                                                                                                                                                                                                                                            LEHR-MASON, Patricia M.
                                                                                                                                                               YUE, Henry
FORSYTHE, Ian J.
MARQUIS, Joseph P.
GIETZEN, Kimberly J.
BAUGHN, Mariah R.
TRAN, Uyen K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TANG, Y. Tom
RANKUMAR, Jayalaxmi
BERELING, Brooke M.
EEE, Erneetine A.
ELLIOTT, Vicki S.
HAFALIA, April J.A.
DUGGAN, Brendan M.
CHAMLA, Narinder K.
BOROWSKY, Mark L.
GRIFFIN, Jennifer A.
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CHANG, Hsin-Ru
KHARE, Reena
BECHA, Shanya D.
                                                                                        Joana X.
Soo Yeun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS FILE REFERENCE: PF-1185 USN CURRENT APPLICATION NUMBER: US/10/489,372 CURRENT FILING DATE: 2004-03-12 PRIOR APPLICATION NUMBER: US 60/322,180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 GCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47.6; DB 20;
Pred. No. 0.00075;
0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7505818CB1
US-10-489-372-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR AFPLICATION NUMBER: US 60/322,100
PRIOR PLING DATE: 2001-09-14
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-09-28
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR PLING DATE: 2001-10-05
PRIOR PLING DATE: 2001-11-02
PRIOR PLING DATE: 2001-11-02
PRIOR PLING DATE: 2001-11-02
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-11-27
PRIOR PLING DATE: 2001-10-06
PRIOR PLING DATE: 2002-10-04
PRIOR PLING DATE: 2002-10-04
PRIOR PLING DATE: 2002-01-04
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-03-18
PRIOR PLING DATE: 2002-05-10
PRIOR PLING DATE: 2002-05-10
PRIOR PLING DATE: 2002-05-10
                                                     RAN, Uyen K.
EHR-MASON, Patricia M.
                                                                                                                                                               RAMKCMAR, Jayalaxmi
EMERLING, Brooke M.
LEE, Brnestine A.
ELLIOTT, Vicki S.
HARPLIA, April J.A.
DUGGAN, Brendan M.
CHAMLA, Narinder K.
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Best Local Similarity 66.7%;
Matches 68; Conservative
    BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shanya D.
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CHANG, Hsin-Ru
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BECHA, Shanye
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JIN, Pei
LEE, Sally
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                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
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78 GCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGT 119

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US-10-489-372-44/c
Sequence 44, Application US/10489372
Publication No. US2004023014A1
GENERAL INFORMATION:
APPLICANT: HONCHELL, CYNTHIA D.
APPLICANT: HONCHELL, CYNTHIA D.
APPLICANT: WARREN, Bridget A.

0; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 TGCACTCGGCCATGTTTGGCTTCTTCTGCAGCTTGGTGTCCAGTCTGAGTCGCTGGTTCC 61
62 TTTGGGGGGGGTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 6.8%; Score 47.6; DB 9; Length 2224;
Best Local Similarity 62.7%; Pred. No. 0.001;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..2224

COTHER INFORMATION: /note= "rat small conductance, calcium-activated potassium channel protein: SEQUENCE DESCRIPTION: SEQ ID NO: 44:

US-09-922-364A-44
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor TTTY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US/09/922,364A
FILLING DATE: 03-Aug-2001
CLASSIFICATION: «UNKNOWN»

PRIOR APPLICATION NUMBER: US/09/254,590
FILLING DATE: 10-Max-1999
APPLICATION NUMBER: US 60/026,451
FILING DATE: 11-SEP-1996
APPLICATION NUMBER: US 60/040,052
FILING DATE: 11-SEP-1997
APPLICATION NUMBER: US 60/040,052
FILING DATE: 17-ARR-1997
APPLICATION NUMBER: US 60/045,233
FILING DATE: 10-ARR-1997
APPLICATION NUMBER: WO PCT/US97/16033
FILING DATE: 10-SEP-1997
ATONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 014210-000730US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 2224 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
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September 8, 2005, 13:43:46; Search time 8202.37 Seconds (without alignments) 3257.733 Million cell updates/sec OM nucleic - nucleic search, using sw model Run on:

US-10-622-407-9 702 1 ttgcactcggccatgtttgg......ttttattgctatgaagtgat 702

Title: Perfect score: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

68479088 Total number of hits satisfying chosen parameters:

34239544 segs, 19032134700 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

9b est1: * 9b est2: * 4 9b est3: * 4 9b est43: * 9b est46: * 9b est6: * 9b es EST:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STHAMBLIES

		di			SUMMARIES	
Result No.	Score	Query Match	o Query Match Length DB	DB	Ü	Description
				; ,		
⊣ .	697	99.3	9/77	n '	AK012838	
~	694	98.9	1003	9	BY711952	BY711952 BY711952
m	602	85.8	765	7	CN461442	CN461442 UI-M-HB0-
4	602	85.8	4224	m	BC076592	BC076592 Mus muscu
'n	573.4	81.7	969	ß	BU611594	BU611594 UI-M-FIO-
9	571	81.3	708	9	CB525851	CB525851 UI-M-FY0-
7	562	80.1	784	9	CB723050	CB723050 UI-M-GH0-
80	539	76.8	683	۲	CF729486	CF729486 UI-M-HD0-
o	403	57.4	410	σ	CG651536	CG651536 OST412784
10	392.4	55.9	415	σ	CG535649	CG535649 OST122794
11	375.8	53.5	639	4	BG077775	BG077775 H3019F06-
12	358.8	51.1	585	~	BB613091	_
13	354.6	50.5	614	٦	CN687949	
14	353.6	50.4		7	CN697902	•
15	316.4	45.1	371	ഹ	BY182663	
16	315.8	45.0	489	7	CK333918	CK333918 H8266D02-
17	304.2	43.3	331	S	BY343934 '	
18	301	42.9		S	BY208766	BY208766 BY208766
19	295	42.0		Ŋ	BY345556	BY345556 BY345556
20	278.4	39.7	410	S	BY183172	BY183172 BY183172
21	266.4	37.9	331	ഗ	BY195969	BY195969 BY195969
22	233.4	33.2	346	2	BY010018	BY010018 BY010018
23	232.8	33.2	347	~	BB873121	BB873121 BB873121
24	229.4	32.7	341	ß	BY036522	BY036522 BY036522

BY325940 BY325940 AI747041 ul12g01.y BY181385 BY181385 BY175331 BY175331 BY187354 BY187354 BY177525 BY177525 BY177525 BY177525 BY27517 RPCI-23-2 AQ27517 RPCI-23-2 AQ405040 IM0173F02 CK634366 Ul-M-HNO-AQ478921 MUB mUBCUL BY365B28 FORWARG B	C82050 C82050 Leuk C82250 C82250 Leuk AU050103 AU050103 AU050106 AU050106 BY748342 BY748342
BY325940 AI747041 BY181385 BY181385 BY17525 BY177525 BY177525 CK6842271 CK688320 CK342400 CK34240 AQ927517 AG405040 CK634366 AG478921 BX969828	C82050 C82250 AU050103 AU050106 BY748342
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3333 3433 3432 3433 2562 2664 2664 2664 2666 2666 2666 2666	742 900 741 747 719
2291. 2291. 2291. 221. 221. 221. 221. 231. 231. 231. 23	122.4 122.4 122.3 12.2 15.2
223 210 210 208.2 208.2 208.2 208.2 193.1 190.2 181.4 1119.4 110.4 110.4	87 87 85.4 80.4
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ALIGNMENTS

AKO12838 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM TITLE JOURNAL MEDLINE PUBMED AUTHORS TITLE AUTHORS TITLE AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS TITLE AUTHORS TITLE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE DUBMED TITLE JOURNAL MEDLINE TITLE JOURNAL MEDLINE DUBMED TITLE JOURNAL AUTHORS TITLE JOURNAL MEDLINE TITLE JOURNAL MEDLINE TITLE JOURNAL MEDLINE TITLE JOURNAL MEDLINE TITLE JOURNAL MEDLINE TITLE JOURNAL AUTHORS TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITLE JOURNAL TITL

5 The FANTOM Consortium and the RIKEN Genome Exploration Research

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JOURNAL

TITLE

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Mus musculus in Marazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dasses I to 1003)
Si Moasaa, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osaro, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brust, V., Cotbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrect, A., Frazer, K.S., Gasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaii, H., Kawasawa, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Matchin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Namata, K., Okido, T., Pavan, W.J., Pettea, G., Pescle, G., Pettovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, J.C., Reed, J.C., Ringwald, M., Ringy, B.Z., Ringwald, M.,
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Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hirawoka,T., Mori,F., Inotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Itoh,M., Izawa,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sano,H., Saskai,D., Shibata,K., Shibata,Y., Sano,H., Sasaki,D., Shibata,Y., Togama,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toga,Y.T., Yamamura,T., Yasunishi,R., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. Yoshida,K., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. Togancal Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Rangawa 210-0045, Japan (E-mail:genome-res@gsc.riken.jp, Rxishitp://genome.gsc.riken.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5, GAGAGAGAGATCCAAGAGCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subsraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter
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/db_xref="G1:263779809"
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Krianslat_ion="MIELHSPKCPAGEYWSKDVCCKNCSAGTPVKAPCEIPHTQGQCE KCHPGTPTEKDNYLDACILCSTCDKODEMVADCSATSDRKCQCRTGLYYYDPKFPESC RPCTKCPQGIPVLQBCNSTANTVCSSSVSRRSASVAWPI"
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/db_xref="PANTOW DB:2810028K06"
/db_xref="tax.on:10090"
/clone="281.0028K06"
/tissue type="whole body"
/clone lib="RISM full-length enriched mouse cDNA library"
/dev stage="10, 11 days embryo"
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Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2276)
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JOURNAL
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AUTHORS
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Matches

8 g ò

SDS

FEATURES

COMMENT

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CN461442 1765 bp mRNA linear EST 21-APR-2004 UI-M-HBO-coy-c-18-0-UI.rl NIH_BMAP_HBO Mus musculus cDNA clone IMAGE:30652769 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencian by: Dr. M. Bento Soares, University of Iowa DNA Sequencian Dy: Dr. M. Bento Soares, University of Iowa DNA Sequencian Dy: Dr. M. Bento Soares, University of Iowa DNA Sequencian Dy: Dr. M. Bento Soares, University of Iowa DNA Sequencian Dy: Dr. M. Bento Soares, University of Iowa Distribution: Distribution information can be found at http://genome.ulowa.edu/distribution/mousefl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 CAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGA 420
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus (bordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 765)

1 (bases 1 to 765)
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                        61 GCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGC 120
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                                                                                                                      121 TATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTG
                                                                                                                                                                                                                                             181 TIGCAAGAACTGITCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCA
                                                                                                                                                                                                                                                                                                                                                                                241 AGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGC
                                                                                       TATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTG
                                                                                                                                                                                                       189 ITGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCA
                                                                                                                                                                                                                                                                                                                           249 AGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             669 TTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT 702
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Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Watlas, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, Z., Zavolan, M., Zhu, Y., Zhimer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komo, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Azawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Genome Encyclopedia Genome Exploration Research Genome Encyclopedia Genome Exploration Research in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIXEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Pax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: genome-ree@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Pukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,P.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Direct Submission
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/dev_stage="10, 11 days embryo"
/clone lib="RIKEN full-length enriched, 10, 11 days
whole body"
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694; Conservative 0; Mismatches
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/clone="2810028K06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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Hus muscoulus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (bases 1 to 4224)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,

Hopkins, R.F., Jordan, H., Mooret, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Morenson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, B., Retteman, M., Madan, A., Rougiques, S.,

Sanchez, A., Whiting, M., Madan, A., Youchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone has the following problem: clone inconsistent with known gene structure.
                                                                                                                                                                                                                                                                                                                                                     BC076592 4224 bp mRNA linear HTC 27-JUL-2004
Mus musculus tumor necrosis factor receptor superfamily, member 22,
mRNA (cDNA clone IMAGE:30652769).
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Debs 51c: http://genome.uiowa.edu
Contract: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Contract: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Stablar,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                            CCTTTGAGTGTGTGCTAATTGTGTCCGTTGTTGTCTTCCGTATCATAAGAAGATAAAGGTTC 624
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg, R. Direct Submission Submitted (06-JUL-2004) National Institutes of Health, Mammalian Submitted (06-JUL-2004) National Institutes
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Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
       human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                  625 TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT 666
                                                                                                              661 TACAGATGTTTTCTTAGCTTCCTTTTATTGCTATGAAGTGAT
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                                                                                                                                                                                                                                                                    /tissue_Trype="whole eye"
/dev_stage="embryo 12.5,13.5,14.5 dpc"
/dev_stage="whole eye"
/dev_stage="whole eye"
/dev_bost="whole eye"
/dev_bost="whole (Ti phage resistant)"
/clone lib="NIH BMAP HBO"
/note="Organ: Bye; Vector: pXx- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel:First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is TTATTGAAGT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITITGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCCTTGCAGGTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 TITCCAGAATCGTGCCGCCCATGTACCAAGGTGTCCCCAAGGAATCCCTGTCCTCCAGGAA 489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATACTCAAGGACAATGTGAGGAGTGTCACCCAGGAACATTCACAGAGAAAAGATAATTAC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601 CCTTTGAGTGTGCTAATTGTGTCCGTTGTCTTCCGTATCATAAGAAGATAAAGGTTC 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 TIGCACTCGCCCATGTTTGGCTTCTTCTGCAGCTGTCTCAGTCTCAGTCTGAGTCGCTGGTTC 69
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                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                     'clone="IMAGE:30652769"
                                                                                                                                                                                                             xref="taxon:10090"
                                    location/Qualifiers
                                                                                                                                               mol_type="mRNA"
strain="C57BL/6"
Seg primer: pYX-5.
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTGTTCTGCA 180
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 CACCCAGGAACATTCACAGAGAAAGATAATTACCTGGATGCTTGTATACTTTGCTCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTACATTTGTCAAGGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGAGAAGGTGT
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                                                                                                                                                                                                                                                                                                                     The following repetitive elements were found in this cDNA sequence: 39-75, >(CAG)n#Simple_repeat (matched compliment) 647-674, >(TAAAA)n#Simple_repeat (matched compliment) Seq primer: pXX-5.
                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.7%; Score 573.4; DB 5;
93.2%; Pred. No. 3.8e-155;
live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    program coordinator."
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Matches 629; Conservative
                                                                                                        Unpublished (1999)
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UI-M-FIO-cav-h-06-0-UI.rl NIH BMAP_FIO Mus musculus CDNA clone
UI.M-FIO-cav-h-06-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                           Length 4224;
                                                                                                                                                                                                       Score 602; DB 3; Length 422.
Pred. No. 3.2e-163;
0; Mismatches 0; Indels
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                                                                                  tissue type="Bye"
/clone lib="NIH BMAP_HB0"
/lab host="DH10B"
                                            /db_xref="taxon:10090"
/clone="IMAGE:30652769"
                                                                                                                                                /note="Vector: pYX-ASC"
      /mol_type="mRNA"
/strain="C57BL/6"
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                                                                                                                                                                                                         tch 85.8%; al Similarity 93.6%; 657; Conservative
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CB525851 708 bp mRNA linear EST 09-JUL-2003
UI-M-FYO-cfe-p-15-0-UI.rl NIH BMAP_FYO Mus musculus cDNA clone
IMAGE:6848608 5', mRNA sequence.
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/tissue_type="whole brain"
/dev_stage="embryo" 13.5,14.5,16.5,17.5dpc"
/lab_host="DHUB (TI phage resistant)"
/clone_lib="NIH BMAP_FYO"
/note="Organ: Brain; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
                                                                                                                                                                                                                                                   480
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                 TGTGATAAAGATCAGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAG
                                                                               TGCCGAACAGGTCTTTACTACTATGACCCAAAATTTCCAGAATCGTGCCGCCCATGTACC
                                                                                                                                                                                          AAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGC
                                                                                                                                                                                                                                                AAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGTCTTCCGTATCATAAGAAGATAAAGGTTCTACAGATGTTTTCTTAGCTTCCTTTA
The following repetitive elements were found in this cDNA sequence: 35-71, > (CAG)n#Simple_repeat (matched compliment) 643-670, > (TAAAA)n#Simple_repeat (matched compliment)
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/strain="C57BL/6"
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TITLE
JOURNAL
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primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecot I adaptor, digested with NotI and then cloned directionally into pXX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University lowa Brain Anatowy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB723050
UI-M-GH0-cel-e-02-0-UI.rl NIH_BMAP_GH0 Mus musculus cDNA clone IMAGE:6841035 5', mRNA sequence.
strand cDNA synthesis was primed with oligo-dT
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                                                                                                                                                                               Length 708;
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                                                                                                                                                                             Score 571; DB 6; I
Pred. No. 1.9e-154;
3; Mismatches 0;
                                                                                                                                        program coordinator."
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CB723050.1 GI:29780192
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llarity 93.3%;
Conservative 0
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
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CF729486.1 GI:37603654
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/dev stage="1, 5, and 15 days newborn"
/lab.host="Blud (Ti phage resistant)"
/lab.host="Blud (Ti phage resistant)"
/clone lib="NIH BMAP GHO"
/clone lib="NIH Brain; Vector: pXx - Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel: First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pXx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
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                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 784)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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/clone="IMAGE:6841035"
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/strain="C57BL/6"
                         Mus musculus (house mouse)
Mus musculus
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CF729486 683 bp mRNA linear EST 09-OCT-2003
UI-M-HDO-cld-d-03-0-UI.rl NIH_BMAP_HDO Mus musculus cDNA clone
IMAGE:30614762 5', mRNA sequence.
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.ulowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
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Was musculus (house mouse)

Mus musculus (bazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.

1. (bases 1 to 683)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                   581 GGCTGTTCCTACTGTTATCACCTTTGAGTGTGCTAATTGTGTGCGTTGTTGTCTTCCGTA
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                                                                  AGGAAATGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTC
                                                                                                                                                                                               TITACTACTATGACCCAAAATTTCCAGAATCGTGCCCCCCATGTACCAAGTGTCCCCAAG
                                                                                                                                                                                                                                                                                                                          461 GAATCCCTGCTCCAGGAATGCAACTCCACAGCTAACACTGTGTGCAGTTCATCTGTTT
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Location/Qualifiers
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/clone="IMAGE:30614762"
/tissue_type="whole eye"
/dev stage="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
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Indiminate, buttering,
Lexicon Genetics Incorporated

OmniBank

JOURNAL

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

Mus musculus (house mouse)

SOURCE ORGANISM

CEYWORDS

REFERENCE AUTHORS

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/clone_lib="NIH BMAP_HD0"

/note="Organ: Bye; Vector: pXX- Asc; Site_l: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
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CG535649 415 bp mRNA linear GSS 01-OCT-2003 OST122794 Mus musculus 1295v/Ev Mus musculus cDNA clone OST122794,
                                     Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
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4000 Research Forest Drive, The Woodlands, TX 77381, USA Email: materials@lexgen.com
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                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                        /cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"
                                                                                                                                                                                                                                                                                                                    57.4%; Score 403; DB 9; Le
100.0%; Pred. No. 1.1e-105;
iive 0; Mismatches 0;
                                                                                                                    1. .410
/organism="Mus musculus"
/mol type="mRNA"
/strain="1295V/Ev"
/db xref="taxon:10090"
/clone="OST412784"
                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100./
Matches 403, Conservative
                                                                              Class: Gene Trap.
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CG651536 410 bp mRNA linear GSS 02-OCT-2003 OST412784 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST412784,

mRNA sequence. CG651536 CG651536.1 GI:37475385

DEFINITION ACCESSION VERSION

RESULT 9 CG651536

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

ORIGIN

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/lone libra Will Mouse 15K CDNA Clone Set"
/clone is among a rearrayed set of 15,247 clones from 11 enbryo cDNA libraries (including preimplanteation stage embryo cDNA libraries (including preimplanteation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT).Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse development cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extrembryonic tissue of 7:5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Institute on Aging/National Institutes of Health 313 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3019 row: F column: 06 Seq primer: -21M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81 GCTGCTGCTGCTGCTGCTGCTGAATCTGCCGGTAAAATTTGCTATGCTAGAATT 140
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 639)

Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Plao, Y., Nagaraja, R., Doi, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
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H3019F06-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone H3019F06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 26, 2001 this sequence version replaced gi:12560343. Other ESTs: H3019F06-3
Contact: George J. Kargul
Laboratory of Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/strain="CS7BL/6G"
/db_xref="niaEST:H3019F06-5"
/db_xref="taxon:10090"
/clone="H3019F06"

    .639
    /organism="Mus musculus"

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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

B. (bases 1 to 415)

S. Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,

Piggott, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A.,

Friddle, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jaing, C.,

Key, B.W. Jr., Kipp, P., Kohlhauff, B., Ma, Z.-O., Markesich, D.,

Payre, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,

Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

Zhu, O., Person, C. and Sands, A.T.

Whall kinase deficiency lowers blood pressure in mice a gene-trap screen to identify potential targets for therapeutic intervention

Droc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AAATTTGCTATGCTAGAATTACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 CTGGATGCTTGTATACTTTGCTCCACCTGTGATAAAGATCAGGAAAATGGTGGCCGACTGC 249
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/clone_lib="Mus musculus 1298v/Ev"
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Location/Qualifiers
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CG535649.1 GI:37322221
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Tayami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

L Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB613091 RIKEN full-length enriched, 10 day neonate skin Mus
musculus cDNA clone 4732455018 5', mRNA sequence.
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Haysehi, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-Cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1677-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
ACACTCCTTCAAATGTCCCGCTGGTGAATACTGGTCTAAAGACGTCTGTTGCAAGAACTG
                                    ATACTCCTACAACTGTCCCGATGGTGAATACCAGTCTAATGATGATGTTGCTAGAGACCTG
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                              encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
                                                                                                                                                     Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RIKEN full-length enriched, 10 day neonate
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Computer-based methods for the mouse full-length cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="skin"
/dev_stage="10 days neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="4732455018"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
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음 ò 용 CN687949

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Seg primer: M13 Reverse
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CN697902
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/tissue type="Embryonic Stem Cell"
/lab host="Nallow"
/lab host="Nallow"
/cell line="129.3 Es cells"
/lab host="Nallow"
/clone lih="NIA Mouse Embryonic Stem (ES) cell (Lif-, 48
h, high density) cDNA library (Long)" | Site 1: Sall;
/note="Wector: pCWW-SPORT6 (Invitrogen); Site 1: Sall;
Site 2: Not1; Mouse cDNA project by the Laboratory of GeneTics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgeun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). ES
cells were plated at density 3x104/cm2, on gelatin-coated
plates and cultured for 48 hrs at 37 OC, $$ CO2. Culture
medium: DNEM supplemented with 15* FBS, 2 mM L-glutamine,
0.1 mM NEAA, lmM Sodium pyruvate, 0.1 mM
beta-mercaptoethanol, 100 U/ml penicillin, and 100 ug/ml
streptomycin. Double-stranded cDNAs were synthesized with
an Oligo (AT) primer [Invitrogen:
Synthesized with 15% trom
                                                                                                                                                                                                                                  614 Dp mRNA linear EST 17-WAY-2004 E0250A07-5 NIA Mouse Embryonic Stem (ES) cell (Lif-, 48 h, high density) cDNA library (Long) Mus musculus cDNA clone NIA:E0250A07 IMAGE30854118 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abarov, A.A., Placo, Y., Matoba, R., Dudekula, D.B., Qian, Y., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., VanBuren, V., Falco, G., Martin, P.R., Stagg, C.A., Bassey, U.C., VanBarg, Y., Carter, M.G., Hamatani, T., Aiba, K., Akuchu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshikawa, T., Jaradat, S.A., Pantano, S., Sochessinger, D., Kolez, E., Kelseo, G., Umezawa, A., Vescovi, A.L., Rossant, J., Klotz, E., Kelseo, G., Umezawa, A., Vuro, M., Kelso, J., Hide, W. and Ko, M.S.
D'Urso, M., Kelso, J., Hide, W. and Ko, M.S.
Transcriptome analysis of mouse stem cells and early embryos PLoS Biol. 1 (3), 410-419 (2003)
418 ATGTACCAAGTGTCCCCAAGGAATCCCTGTCCTCCAGGAATGCAACTCCCCAAGTTAACA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |mol_type="mRNA"
|strain="129Sv/EvTac"
|db_xref="niaEST:E0250A07-5"
|db_xref="taxon:10090"
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Plate: E0250 row: A column: 07
Seq primer: M13 Reverse
High quality sequence stop: 614
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                                                                                CTGTGTGCAGTTCATCTTTTCAAA 503
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AUTHORS
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FEATURES

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Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAS were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORTE plasmid vector. The DH10B E. coli host was transformed with the lightion mixture by the standard chemical method. The average insert size is about 3.4 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AATACCAGTCTAATGATGTCTGTTGCAAGACCTGTCCCTCAGGTACATTTGTCAAGGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 TGGTGGCTGACTGTTCTGCCGCCAGTGACCGGAAATGCGAGTGCCAAATAGGTCTATACT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 CCTGCAAAATCCCCCATACTCAAGGACAATGTGAGAAGTGTCACCCAGGAACATTCACAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 TGGTGGCCGACTGCTCAGCCACCAGTGACCGGAAATGCCAGTGCCGAACAGGTCTTTACT 406
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 597)
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                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 614;
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Pred. No. 1.4e-91;
0; Mismatches 39;
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.5%;
Best Local Similarity 90.6%;
Matches 378; Conservative
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                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /notes "Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall;
Site_2: Not1; Mouse cDNA project by the Laboratory of
Genefics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref.
Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 3 embryos at 11.5-days
postcoitum. Double-stranded cDNAs were synthesized with an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 AGGTAATATTTGCTATGCCTGAATCATACTCCTTCAACTGTCCCGATGGTGAATACCAGT 156
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                                                                                                                                                                                  /db_xrefe="teaxon:10090"
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/tissue type="whole embryo including extraembryonic tissues at 11.5-days postcoitum"
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                                                                                                                                                                 db_xref="niaEST:E0401A05-5"
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose washetance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/cloll type="NOD-derived CD11c +ve dendritic cells"
/clone lib="RENF full-length enriched, NOD-derived CD11c +ve dendritic cells"
Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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0; Mismatches 20; Indels 0
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                                                                                                                                                                                                                              Location/Qualifiers
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Sequence 57, Appl Sequence 27, Appl Sequence 21, Appl Sequence 1, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 46, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 25, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl	### and Characterization of superfamily suber of the TNP-Receptor Superfamily by the TNP-Receptor Superfamily sets;	Characterization of of the TNF-Receptor Superfamily
US-08-050-319B-57 US-08-465-982-57 US-08-68-683A-21 US-10-125-062-1 US-10-125-062-1 US-08-794-022-46 US-08-794-45A-46 US-08-795-447A-46 US-08-795-447A-46 US-08-795-447A-46 US-08-795-447A-46 US-08-795-446B-46 US-08-795-446B-46 US-08-795-798C-46 US-08-50-70-78BC-13 US-09-50-313A-13 US-09-50-313B-25 US-08-321-668-2 US-08-321-668-2 US-08-321-668-2 US-08-321-668-2 US-08-321-668-2	IGNMENTS B tification 627199e1 M 12,033B ,063 re 1008; d. No. 7.4 ismatches	612033B n, Identification, and a No. 6627199el Member ss us/09/612,033B
167 1 167 1 167 1 167 1 167 1 167 2 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		on US/096 ris Isolation tmat2, a of Genes 7/35434A
	SULT 1 -09-612-033B-10 Sequence 10. Application US/09612033 Batent No. 6627199 GENERAL INFORMATION: Selation, Iden TITLE OF INVENTION: Emalt, a No. 6 TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: Of Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF INVENTION: OF Genes TITLE OF GENES TITLE OF INVENTION: OF Genes TITLE OF GENES TITLE OF INVENTION: OF Genes TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENES TITLE OF GENE	SULT 2 Sequence 8, Application US/0961203 Sequence 8, Application US/0961203 Patent No. 6627199 GENERAL INFORMATION: APPLICANT: Saris, Chris TITLE OF INVENTION: Insolation, Id TITLE OF INVENTION: of Genes FILE REFERENCE: 01017/35434A CURRENT APPLICATION NUMBER: US/09
2011.5 2011.5 2011.5 2011.5 2011.5 2011.5 2011.5 2011.5 2011.5 2011.5 2011.5	ULT 1 09-612-0338-1 equence 10, A attent No. 662 ENERAL INFORM APPLICANT: Sa APPLICANT: Sa TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE TITLE OF INVE CURRENT FILING NUMBER OF SEQ SOFTWARE: PAL SOFTWARE: PAL SOFTWARE: PAL OF 10 10 10 LENGTH 180 LENG	SULT 2 -09-612-033B-8 Sequence 8, App. Patent No. 6627 GENERAL INFORMA APPLICANT: SAT. TITLE OF INVENTITLE REFERENCE CURRENT APPLIC
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Parent No. 6627199
GENERAL INFORMATION:
APPLICANT: Saris, Chris
TITLE OF INVENTION: Lasts, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: of Genes
TITLE OF INVENTION: of Genes
TITLE OF INVENTION: of Genes
TITLE OF INVENTION: a GONES
TITLE OF INVENTION: of Genes
FILE REPERENCE: 01017/35434A
CURRENT PILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PARENT PILING DATE: 2000-07-09
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Patent No. 6271366

GENERAL INFORMATION:
APPLICANT: Kimura, Naoki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 06501/0408/0411,722
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT PILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: DCT/DP98/01511
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR FILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
FENOUND 11
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         Sequence 6, Application US/09612033B
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ORGANISM: Mus musculus
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Best Local Similarity
Matches 133; Conserv
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Matches 131; Conserv
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US-09-411-722-1
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APPLICANT: Saris, Chris
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: tmst2, a No. 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: of 6627199e1 Member of the TNF-Receptor Superfamily
TITLE OF INVENTION: 0.6627199e1 Member of the TNF-Receptor Superfamily
FILE REFERENCE: 01017/35434A
CURRENT APPLICATION NUMBER: US/09/612,033B
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
LENGTH: 398
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US-09-612-0338-14
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                                                                                                                                                                                                                                                                          Length 198;
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Pred. No. 6.9e-83;
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                                                                                                                                                                                                                                                      94.8%; Scc. No. 100.0%; Pred. No. 0, Mismatches
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-612-033B-14; Sequence 14, Application US/09612033B; Patent No. 6627199; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 170; Conservative
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                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
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US-09-612-033B-8
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                                                                                                                                                LENGTH: 198
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Best Local 9
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Gaps ;

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67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
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                                                                                                                                                                                            5 SHVSSLSHWF------LILLINIFIPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG
                                                                                                                               Length 176;
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RESULT 4 US-09-612-033B-6

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39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD
                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09855266A Patent No. 6784284; GENERAL INFORMATION:
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Matches 112; Conservative
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US-09-855-266A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2. Application US/09411722
Patent No. 6271366
GENERAL INFORMATION:
PAPLICANT: Kimura.
PAPLICANT: Kimura.
PILE REPERREC: 06501/04001
CURRENT APPLICATION NUMBER: US/09/411,722
CURRENT FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/UP98/01511
PRIOR APPLICATION NUMBER: PCT/UP98/01511
PRIOR APPLICATION NUMBER: 1999-04-01
PRIOR PILING DATE: 1997-04-01
PRIOR FILING DATE: 1997-04-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 148
                                                                                                                                                                         APPLICANT: TOYOSHIMA, TOMOKI
APPLICANT: TOYOSHIMA, TOMOKO
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 06501-040002
CURRENT PILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR PLING DATE: 1999-10-01
PRIOR PILING DATE: 1999-10-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1999-04-01
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 176
                                                                                                                      ; Sequence 1, Application US/09855266A; Patent No. 6784284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 79.9
Matches 131; Conservative
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Matches 112; Conservative
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CRGANISM: Mus musculus
US-09-411-722-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Mus musculus
                                                                                                                                                            GENERAL INFORMATION:
                                                                                 RESULT 6
US-09-855-266A-1
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US-09-411-722-2
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61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQBCN 120
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                                                                                         158
                                                                                                                       61 DCELCSTCDKDQNWVADCSATSDRKCECQIGLYYYDPKFPSCRPCTKCPQGIPVLQBCN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD
                                                                                         99 ACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKPPESCRPCTKCPQGIPVLQECN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09855266A

Sequence 13, Application US/09855266A

Sequence 13, Application US/09855266A

Sequence 13, Application US. 6784284

GENERAL INFORMATION:
APPLICANT: Kimura, Naoki

TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPERENCE: 06501-040002

CURRENT APPLICATION NUMBER: US/09/855, 266A

CURRENT FILING DATE: 1099-10-01

PRIOR FILING DATE: 1999-10-01

PRIOR FILING DATE: 1999-0-01

PRIOR PLING DATE: 1998-04-01

PRIOR PLING DATE: 1998-04-01

PRIOR PLING DATE: 1998-04-01

HORDER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: INFORMATION:
APPLICANT: TOYOSHIMA, TOMOKI
APPLICANT: TOYOSHIMA, TOMOKO
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-04002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US/9411,722
PRIOR APPLICATION NUMBER: US/99/11,722
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: US/99-03
PRIOR APPLICATION NUMBER: US/99-01
PRIOR APPLICATION NUMBER: US/99-053
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: US/99-053
PRIOR FILING DATE: 1997-04-01
SEQ ID NOS: 13
COFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 2
LENGTH: 148
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US-09-006-353A-14
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                                                                                                                                                                                                       48 CPAGEY---WSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCS 104
                                                                                                                                                                                                                                                                                                              61 TCRKEMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNG-TVTIPCKETQ 119
                                                                                                                                                                                                                                                                                  105 TCDKD--QEMVADCSATSDRKCQCRTGLYY-YDPKFPESCRPCTKCPQGIPVLQECNSTA 161
                                                                                                                                                                                                                               1 CPGGKYVHSKNNSICCTKCHKGTYLVSDCPSPGRDTVCRECEKGTFTASQNYLRQCLSCK 60
                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08292549
Patent No. 5464938
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
                                                                                                                                                                   59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.7%; Score 208.5; DB 1;
33.8%; Pred. No. 6.5e-12;
tive 21; Mismatches 68;
                                                                                                                              21.1%; Score 212.5; DB 4 34.7%; Pred. No. 8.4e-13; iive 15; Mismatches 59
SOFTWARE: FastSEQ for Windows Version 4.0
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,330
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION:
NAME: PERKINE, PARKINE, CASO, STELEPHONE: (206) 233-0644
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 355 amino acids
amino acid
                                                                                                                          Query Match
Best Local Similarity 34.7'
Matches 43; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seattle
: Washington
RY: USA
                                                                       ORGANISM: Mus musculus
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Best Local Similarity
Matches 51; Conserv
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                                                                                          US-09-855-266A-13
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                 SEQ ID NO 13
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80 GOCEKCHPGTFTEKDNYLDACILCS-TCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFP 138
                                                                         63 TQCTPCASDTFTSRNNHLPACLSCNGRCDSNQVETRSCNTTHNRICDCAPG-YYCFLKGS 121
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7 LLLLSCIIIINSDITPH----EPSNGKCKDNEYKRHHLCCLSCPPGTYASRLCDSKTNTN 62
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                                                                                                                                                                                                                                                                                                       APPLICANT: YU, GRO-LIANG
APPLICANT: TU, GRO-LIANG
APPLICANT: RUBEN, STEVEN
TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,353A
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Pred. No. 6.5e-12
                                                                                                                                           139 ESCRPC---IKCPQGIPVLQECNSTANTVCS 166
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Patent No. 6261801
GENERAL INFORMATION:
APPLICANT: WEL, YING-FEI
APPLICANT: YU, GUO-LIANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELLING LALES:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9F341
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8514
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
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RESULT 12 US-09-573-986-14

21 LLLLLLLLLLLLLLLVPPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEI-PHTQ 79

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20.6%; Score 207.5;
    TELEPHONE: (202) 628-5197
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amino acid
  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                        MOLECULE TYPE: protein US-08-804-166-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-910-991-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-910-991-6
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                                                                                                                                                                                                                                                                                                                                                                                                                 11; Gaps
                                                                                                                                                                                                                                                                                                                                                                    20.7%; Score 208.5; DB 4; Length 355; 33.8%; Pred. No. 6.5e-12;
                                                                                                                                                                                                                                                                                                                                                                                                             68; Indels
                                                    APPLICANT: Wei, Ying-Fei
APPLICANT: Wei, Jian-Fei
APPLICANT: Ni, Jian APPLICANT: Reiner
APPLICANT: Ruben, Steven
TITLE OF INVENTION: Tumor Necrosis Factor Receptor 5
FILE REFERENCE: 1488,1280004
CURRENT APPLICATION NUMBER: US/09/573,986
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 22207
ZIP: 22207
ZIP: 22207
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALUKESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 ESCRPC---TKCPQGIPVLQECNSTANTVCS 166
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                                                                                                                                                                                                                                                                                                                                                                                                             21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CAMPBELI
TELEPHONE: (202) 628-5197
TELEPHONE: (202) 628-5197
Sequence 14, Application US/09573986
Patent No. 6455040
                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
                                                                                                                                                                                                                                                   SEQ ID NO 14
LENGTH: 355
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                  US-09-573-986-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-08-804-166-6
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57 PGQDTDCRECESGSFTASENHLRHCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRH 116
                                                                                                                                                                                                                       76 PHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTGLY-Y 132
                                                                                                              20 RILLILLILLILLILLINDP-LQVKPAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFVKAPCEI 75
                                                                                                                                                                 2 RTSLLLAFGLLCLPWLQEGSA----DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPG 56
Query Match 20.6%; Score 207.5; DB 3; Length 285; Best Local Similarity 34.4%; Pred. No. 6.3e-12; Matches 53; Conservative 17; Mismatches 71; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/910,991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                     117 YMSENLFQCFNCTLCLNG-TVHLSCQEKQNTVCT 149
                                                                                                                                                                                                                                                                                                                                   133 YDPKFPESCRPCTKCPQCIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: YUN, Allen C.
REGISTATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CAMPBELL=2B
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08910991
Fatent No. 6194177
GENERAL INFORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Chappel, Scott C.
TITLE OF INVENTION: HYBRID PROTEINS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE: 20 February 1997
PRIOR APPLICATION NUMBER: 60/011,936
FILING DATE: 20 February 1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 PHIQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSAFSDRKCQCRTGLY-Y 132
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                                                                  20 RLLLLLLLLLLLLLLLVRP-LQVKFAMLELHSFKCPAGEY---WSKDVCCKNCSAGTFVKAPCEI 75
                                                                                                     2 RTSLLLAFGLLCLPWLQEGSA-----DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 RISLILAFGLICLPWLQEGSA----DSVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPG 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.6%; Score 207.5; DB 4; Length 285; 34.4%; Pred. No. 6.3e-12; Live 17; Mismatches 71; Indels 13; Gaps
                            13;
                         71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22207
COMPUTER READABLE FORM:
MEDIUM TYRE. Floppy disk
COMPUTER: Floppy disk
COMPUTER: TEM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,186
34.4%; Pred. No. 6.3e-12; tive 17; Mismatches 71
                                                                                                                                                                                                                                                              133 YDPKFPESCRPCTKCPOGIPVLOECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                               117 YWSENLFQCFNCTLCLNG-TVHLSCOEKONTVCT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAMPBELL=2A
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09756186
Patent No. 6663867
GENERAL INPORMATION:
APPLICANT: Campbell, Robert K.
APPLICANT: Campbell, Scott C.
TITLE OF INVENTION:
TITLE OF INVENTION:
HYBRID PROTEINS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIPICATION:
ATTCRNEY/AGRAT INFORMATION:
NAME: Browdy, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: 25,618
TELECOMMUNICATION INFORMATION:
TELEFRAX: (202) 628-5197
TELEFRAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 amino acids
TYPE: amino acid
TYPE: ..., inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/804,166
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 34.4%
Matches 53; Conservative
                         53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear; MOLECULE TYPE: protein US-09-756-186-6
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-09-756-186-6
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                      Matches
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Search completed: September 9, 2005, 09:35:54 Job time: 117.19 secs

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September 9, 2005, 08:34:50; Search time 548.095 Seconds (without alignments) 129.535 Million cell updates/sec
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1 MFGFFCSLVSSLSRWFLWRR......ANTVCSSSVSRRSASVAWPI 180
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                  OM protein - protein search, using sw.model
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-622-407-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
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Perfect score:
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                                                                                                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 10, Appl	Sequence 8, Appli	Sequence 14, Appl	Sequence 6, Appli	Sequence 14, Appl	Sequence 1, Appli	Sequence 8, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 6, Appli
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	Query Match Length DB	180	198	398	133	396	176	176	176	148	148	117
de	Query Match	100.0	94.8	94.8	74.2	70.3	69.8	6.69	6.69	63.6	63.6	46.3
	Score	1008	926	926	748	709	705	705	705	641	641	467
	Result No.	1	7	e	4	ß	9	7	80	σ	10	11

6 10, 6 3, 13, 14,	4 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114 A 114	Sequence 41, App Sequence 21, Appl Sequence 12, Appl Sequence 12, Appl Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli	
14 US-10-193-616-10 15 US-10-410-012-3 16 US-10-799-345-24 9 US-09-855-266A-13 16 US-10-802-332-13 9 US-09-826-212-14	9 9 9	14 US-10-218-102-423 16 US-10-748-112-21 9 US-09-899-429A-18 9 US-09-756-186-2 16 US-10-724-226-2 9 US-09-756-186-2 16 US-10-724-226-4 16 US-10-724-226-4	9 US-09-756-186-8 16 US-10-724-226-8 9 US-09-899-422-15-9 9 US-09-899-428-25-9 9 US-09-899-428-25-9 9 US-09-999-428-15-9 9 US-09-798-788-11-9 14 US-10-218-102-421 14 US-10-218-102-431 15 US-10-380-438-1
24 4 5 4 4 5 4 4 5 4 4 5 4 4 5 4 4 5 4 4 5 4 4 5 4 4 5 4 5 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	355 355 285 162 162	162 190 200 256 307	336 336 461 461 162 162 162 162 162 162
21.6 21.6 21.6 21.1 21.1 20.7	7.002 2002 2002 2003 4.4.6.0	00000000000000000000000000000000000000	000000000000000000000000000000000000000
217.5 217.5 217.5 212.5 212.5 208.5	208.5 208.5 2007.5 2007.5 2007.5 2007.5	204.5 204.5 204.5 204.5 203.5 203.5 203.5	203.5 203.5 203.5 203.5 202.5 202.5 202.5 202.5 202.5 202.5
122 133 14 14	18 22 22 24 24 25 25	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩ ₩

ALIGNMENTS

RESULT 1

US-10-622-407-10; Sequence 10, Application US/10622407; Publication No. US20040018544A1	ion US/10622407 40018544Al
; GENERAL INFORMATION: ; APPLICANT: Saris, Chris ; TITE OF INVENTION: ISO	ENEGAL INFORMATION: APPLICANT: Saris, Chris TTTIR OF INVENTION ISOLATION. IDENTIFICATION. AND CHARACTERIZATION OF TMST2, A NOVEL
; TITLE OF INVENTION:	TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES
; FILE REFERENCE: 01017/35434B ; CURRENT APPLICATION NUMBER:	FILE REFERENCE: 01017/35434B CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2003-07-17	2003-07-17 MREB: ITS 09/612 033
; PRIOR FILING DATE: 2000-07-07	000-07-07
, PRIOR APPLICATION NUMBER: US 60/143,063	MBER: US 60/143,063
; PRIOR FILING DAIE: 1999-07-09	15 15
; SOFTWARE: PatentIn Ver. 2.0	er. 2.0
SEQ ID NO 10	
; TYPE: PRT	
; ORGANISM: Mus musculus US-10-622-407-10	lus
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 . 000 .
Query Match Rest Local Similarity	100.04; SCORE 1004; UB 13; Deligni 100; 100.08; Pred. No. 5.98-81;
Matches 180; Conservative	rative 0;
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Qy 61 KNCSAGTFVK	61 KNCSAGTFVKAPCEIPHTOGOCEKCHPGTFTEKDNYLDACILCSTCDKDOEMVADCSATS 120
Db 61 KNCSAGTFVK	

N

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Sequence 6, Application US/10622407; Bequence 6, Application US/10622407; Publication No. US200400185441
GENERAL INFORMATION:
APPLICANT: SATIS, Chris
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TWST2, A NO TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUBERFAMILY OF GENES
TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUBERFAMILY OF GENES
FILE REFERENCE: 01017/35434B
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 6
LENGTH: 133
                                                                                                                                                                                                                       61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                         61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
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                                                                                                                                                1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCC 60
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                                                                                                                 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
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Fublication No. US2030096355A1
GENERAL INFORMATION:
APPLICANT: Zhang, Ke
TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: WAZ5, a novel
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
TITLE OF INVENTION: MORBER: US/10/193,616
CURRENT APPLICATION NUMBER: US/10/193,616
CURRENT FILING DATE: 2002-07-11
FRIOR FILING DATE: 2000-07-07
FRIOR FILING DATE: 1999-07-07
FRIOR FILING DATE: 1999-07-07
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     94.8%; Score 956; DB 15; Length 398;
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                            Pred. No. 4.9e-76;
                      100.0%; Pred. ...
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Query Match
Best Local Similarity 100.0
Matches 170; Conservative
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Best Local Similarity
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TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
TITLE OF INVENTION: MEMBER OF THE TWF-RECEPTOR SUPERFAMILY OF GENES
FILE REFERENCE: 0101/354348
CURRENT APPLICATION NUMBER: US 09/612,407
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 09/612,033
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATCHLIN Ver. 2.0
SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                              APPLICANT: Saris, Chris
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TWST2, A NOVEL
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TWST2, A NOVEL
TITLE OF INVENTION: 01017/35448
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
PRIOR PILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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                                                           121 DRKCQCRIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSASVAWPI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
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94.8%; Score 956; DB 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-76;
Matches 170; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10622407
Publication No. US20040018544A1
GENERAL INFORMATION:
                                                                                                                                                                                                              ; Sequence 8, Application US/10622407; Publication No. US20040018544A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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; ORGANISM: Mus musculus
US-10-622-407-8
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                                                                                                                                                                                                                                                                                                           Query Match 70.3%; Score 709; DB 14; Length 396; Best Local Similarity 78.6%; Pred. No. 2.8e-54; Matches 132; Conservative 6; Mismatches 22; Indels
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Fatent No. US20020128435A1
GENERAL INFORMATION:
APPLICANT: Kimura, Naoki
FILE REFERENCE: O6501-040002
CURRENT APPLICATION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: O6501-040002
CURRENT FILING DATE: 2001-05-14
FRIOR APPLICATION NUMBER: US/09/855,266A
CURRENT FILING DATE: 1999-10-01
FRIOR PILING DATE: 1999-10-01
FRIOR PILING DATE: 1998-04-01
FRIOR PILING DATE: 1998-04-01
FRIOR PILING DATE: 1998-04-01
FRIOR PILING DATE: 1998-04-01
FRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                   ) OTHER INFORMATION: ymkz5-Fc fusion protein US-10-193-616-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity 79.9
Matches 131; Conservative
                                                                                                                               TYPE: PRT ORGANISM: Mus musculus
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US-09-855-266A-1
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                                SOFTWARE: Pa
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                                                                                                                                                                                         FEATURE:
                                                                                              LENGTH:
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; Sequence 8, Application US/10193616; Publication No. US20030096355A1

US-10-193-616-8

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67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
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TITLE OF INVENTION: Isolation, Identification, and Characterization of TITLE OF INVENTION: ymkz5, a novel TITLE OF INVENTION: ymkz5, a novel TITLE OF INVENTION: member of the TNF-Receptor Supergene Family FILE REPERBUCE: 01017/35551A CURRENT PAPLICATION NUMBER: US/10/193,616 CURRENT FILING DATE: 2002-07-11 PRIOR PAPLICATION NUMBER: US/09/611,989 PRIOR PILING DATE: 1999-07-07 PRIOR APPLICATION NUMBER: US 60/143,137 PRIOR PILING DATE: 1999-07-07 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver. 2.0 SSEQ ID NO 8 SEQ ID NO 8 SEQ ID NO 8 SEQ ID NO 8
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Sublication No. US20040152879A1

GENERAL INFORMATION:
APPLICANT: Kimura, Nacki
APPLICANT: Tyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REPREBENCE: 06501-040002
CURRENT PILING DATE: 2004-03-16
FRICA APPLICATION NUMBER: US/10/802,332
CURRENT FILING DATE: 2004-03-16
FRICA APPLICATION NUMBER: US/09/855,266
FRICA PAPLICATION NUMBER: US/09/855,266
FRICA FULING DATE: 1999-10-01
FRICA FULING DATE: 1999-10-01
FRICA FULING DATE: 1999-10-01
FRICA FULING DATE: 1998-04-01
FRICA FULING DATE: 1908-04-01
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Pred. No. 2.9e-54;
5; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
69.9%; Score 705; DB 14;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20:
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Best Local Similarity 79.9
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Mus musculus
US-10-193-616-8
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                                                                                                                                                                 Matches 112;
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           TYPE: PRT
                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
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                                                                                                               127 RIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/10802332

Sequence 2, Application US/10802332

Publication No. US20040152879A1

GENERAL INPORMATION:
APPLICANT: Kimura, Naoki

TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002

CURRENT FILING DATE: US/10/802,332

CURRENT FILING DATE: US/09/855,266

PRIOR APPLICATION NUMBER: US/09/855,266

PRIOR APPLICATION NUMBER: US/09/855,266

PRIOR APPLICATION NUMBER: US/09/855,266

PRIOR APPLICATION NUMBER: US/09/855,266

PRIOR PILING DATE: 1999-10-01

PRIOR PILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

PRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1998-04-01

SPRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1999-04-01

SPRIOR FILING DATE: 1998-04-01

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APPLICANT: TOYOSHIMA, TOMOKO
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT FILING DATE: 2001-05-14
PRIOR APPLICATION NUMBER: US 09/411,722
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR APPLICATION NUMBER: PCT/JP98/01511
PRIOR APPLICATION NUMBER: D9 9/099653
PRIOR APPLICATION NUMBER: JP 9/099653
PRIOR APPLICATION NUMBER: JP 9/099653
SPOPWARE: FASELSEQ for Windows Version 4.0
SEQ ID NOS: 13
                                                                                                                                                                                                                                                                  Sequence 2, Application US/09855266A Patent No. US20020128435A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 63.6
Best Local Similarity 84.8
Matches 112; Conservative
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US-09-855-266A-2
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US-09-855-266A-2
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61 DCELCSTCDKDQNWVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
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                                                                                                                                                                                                                                                                                                       99 ACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECN 158
                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Isolation, Identification, and Characterization of TITLE OF INVENTION: ymkz5, a novel TITLE OF INVENTION: ymkz5, a novel TITLE OF INVENTION: member of the TNF-Receptor Supergene Family FILE REFERENCE: 01017/35551A CURRENT APPLICATION NUMBER: US/10/193,616 CURRENT APPLICATION NUMBER: US/09/611,989 PRIOR PILING DATE: 2002-07-11 PRIOR APPLICATION NUMBER: US 60/143,137 PRIOR APPLICATION NUMBER: US 60/143,137 PRIOR PILING DATE: 1999-07-07 NUMBER OF SEQ ID NOS: 15 SOFTWARE: Patentin Ver: 2.0 SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 SHVSSLSHWF-----LLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG 56
                                                                                                                                                                                                                             1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH
                                                                                                                                                                                             39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 SLVSSLSRWFLWRRLLLLLLLLLLLLLDQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
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TITLE OF INVENTION: Isolation, Identification, and Characterization of
TITLE OF INVENTION: ymkz5, a novel
TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
FILE REFERENCE: 01017/35551A
CURRENT APPLICATION NUMBER: US/10/193,616
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                                                                                Score 641; DB 16; Length 148;
Pred. No. 1.1e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.3%; Score 467; DB 14; Length 117; 73.6%; Pred. No. 1.8e-33; tive 5; Mismatches 19; Indels E
                                                                                                                                       15; Indels
                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 10, Application US/10193616; Publication No. US20030096355A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 6, Application US/10193616; Publication No. US20030096355A1; GENERAL INFORMATION:
                                                                                63.6%;
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Best Local Similarity 73.0%
The B9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 STANTVCSSSVS 132
                                                                                                                                       Conservative
; ORGANISM: Mus musculus US-10-802-332-2
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CRCANISM: Mus musculus
US-10-193-616-6
                                                                                                                Best Local Similarity
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11 DCPSPGRDTVCRECEKGTFTASQNYLRQCLSCKTCRKEMSQVBISPCQADKDTVCGCKEN 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 PCBIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCTKCHKGTYLVS 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 LLLLLLLLLLLLLLN-----PLQVKFAMLELHSFKCPAGEY---WSKDVCCKNÇSAGTFVKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 13; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
                     SEQUENCE TO NO. 24 APPLICATION US/10/59345

Publication No. 102004020931641

GENERAL INFORMATION:
APPLICANT: Christopher T. Ritchlin
APPLICANT: Christopher T. Ritchlin
APPLICANT: Bayard Schwarz
TITLE OF INVENTION: Methods and Compositions Related to
TITLE OF INVENTION: Methods and Compositions Related to
TITLE OF INVENTION: Methods and Compositions Related to
TITLE OF INVENTION: Mothods and Composition Diseases
FILE REFERENCE: 21108.0031U2
CURRENT APPLICATION NUMBER: US/10/799,345
CURRENT APPLICATION NUMBER: 60/454,573
FRIOR PILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
TUPE: PRT
TUPE: PRT
TYPE: PRT
TYPE: PRT
SEATURE:
FEATURE:
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APPLICANT: KIMLIA, Naoki
APPLICANT: Toyoshima, Tomoko
TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
FILE REFERENCE: 06501-040002
CURRENT APPLICATION NUMBER: US/09/855,266A
CURRENT FILING DATE: 2001-05-14
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1999-04-01
PRIOR FILING DATE: 1997-04-01
SOUTHARE OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130 LYY-YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 OFORYLSETHFOCVDCSPCFNG-TVTIPCKETONTVCN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.6%; Score 217.5; DB 16; Best Local Similarity 32.3%; Pred. No. 6.5e-11; Matches 51; Conservative 19; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.1%; Score 212.5; DB 9;
34.7%; Pred. No. 5e-11;
tive 15; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09855266A Patent No. US20020128435A1 GENERAL INFORMATION:
      Application US/10799345
No. US20040209316A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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LENGTH: 123
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| Publication No. US2030228276A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Fisel, Ulrich L M
| TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
| TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
| TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
| TITLE OF INVENTION: NEUROPROTECTION VUMBER: US/10/410,012
| CURRENT APPLICATION NUMBER: US/10/410,012
| CURRENT FILING DATE: 2003-04-09
| PRIOR APPLICATION NUMBER: US 60/370,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 PCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 LSLVLLALLMGIHPSGVTGLVPSLGDREKRDSLCPQGKYVHSKNNSICCTKCHKGTYLVS 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.6%; Score 217.5; DB 14; Length 247; 32.3%; Pred. No. 3.6e-11; tive 19; Mismatches .75; Indels 13;
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; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: TNFR1
US-10-193-616-10
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mus musculus
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TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
Matches 51; Conserv
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US-10-799-345-24
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US-10-410-012-3
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us-10-622-407-10.rpr

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

September 9, 2005, 06:50:20; Search time 130.476 Seconds (without alignments) 132.737 Million cell updates/sec

US-10-622-407-10 1008 1 MFGFFCSLVSSLSRWFLWRR......ANTVCSSSVSRRSASVAWPI 180 Title: Perfect score: Sequence:

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		tumor necrosis fac	hypothetical prote	gene G4R protein -	G2R protein - vari	tumor necrosis fac	tumor necrosis fac	OX40 antigen precu	Fas antigen precur	nerve growth facto	apoptosis-mediatin	FAS soluble protei	death receptor-6 -	apoptosis-mediatin	nerve growth facto	nerve growth facto	tumor necrosis fac	T2 protein - rabbi	T2 protein - myxom		. CD27 antigen precu	tumor necrosis fac	gene murine tumour	antigen	н			laminin beta-1 cha	B cell-associated
SUMMARIES	ΩΙ	GQMST1	GQRTT1	T28623	D36858	D72175	GQHUT1	JC4302	S12783	JC2395	COHON	A46484	137383	JC7705	A40036	JN0006	A26431	A35356	B43692	GQVZML	148700	A46517	B38634	I48854	A42086	A49053	I54182	137552	MMFFB1	A46476
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	Length	454	461	348	349	349	455	461	271	324	427	327	314	651	332	416	425	461	325	326	272	260	474	459	592	250	435	277	1790	305
de	Query Match	21.6	20.3	20.0	20.0	20.0	20.0	19.9	18.7	18.7	18.7	18.2	18.1	17.9	17.9	17.5	17.4	17.2	17.2	16.6	16.2	15.6	15.3	14.9	14.9	14.8	14.8	14.2	12.5	12.1
	Score	217.5	204.5	201.5	201.5	201.5	201.5	200.5	188	188	188	183	182	180.5	180	176.5	175	173.5	173	167.5	163.5	157.5	154.5	150	150	149.5	149.5	143	126	122
	Result No.	1	7	m	4	2	9	7	80	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

membrane glycoprot	lymphocyte activat	laminin alpha 5 ch	perlecan precursor	major surface-labe	T-cell antigen 4-1	variant-specific s	laminin B2t chain	epidermal growth f	hypothetical prote	trophozoite surfac	laminin gamma-1 ch	heparan sulfate pr	laminin beta-2 cha	serine proteinase	laminin gamma 2 ch
JC5486	138426	T10053	A38096	A35502	B32393	A48434	A44018	JC4387	T34288	A48579	MMHUB2	S18252	MMRTS	S34583	000698
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493	255	3635	4391	713	256	557	1193	1339	1827	667	1609	3707	1801	1548	1192
12.0	11.8	11.8	11.7	11.5	11.4	11.4	11.4	11.3	11.2	11.2	11.2	11.1	11.1	11.0	10.9
121	119	119	118	115.5	115	115	114.5	114	113	112.5	112.5	112	111.5	111	110
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

	RESULT 1
	ognali tumor necrosis factor receptor 1 precursor - mouse N/Alternate names: tumor necrosis factor receptor, 55K
	C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
	C;Accession: A38634; B40254; S16677; S19021; I54532; I57826 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, B.)
	FIGG. Nacl. Acad. Sci. 0.5.A. 80, 28307-2834, 1931 Aritle: Cloning and expression of CDNAs for two distinct murine tumor necrosis factor r.
-	A;Kererciice number: A30034; MolD:3110/003; FMLD:10132/0
	A;Molecule type: mRNA A;Residues: 1-454 <lew></lew>
	A;Cross-references: UNIPROT:P25118; GB:M60468; NID:g199825; PIDN:AAA39751.1; PID:g199826 R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
	Mol. Cell. Biol. 11, 3020-3026, 1991
	A40254; MUID:91246168; PMID:1645445
	A,Accession: B40254
	A:Residues: 1-454 <co2></co2>
	R.Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissonerghis, A.M.; Gray, P.W.; Feldman
	Eur. o. Infimulation. Lat. 1097-100-0, 1204. A.Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis
	A;Reference number: \$16677; MUID:91285014; PMID:1647956
•	A; Accession: S16677
	A:MOLECULE CYDE: MIKNA A:Meaidhea: 1-454 cBAR>
	A;Cross-references: EMBL:X59238; NID:g53578; PIDN:CAA41922.1; PID:g53579
	R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.
	Immunogenetics 34, 338-340, 1991. Immunogenetics At 338-340, 1991. Immunogenetics to the mouse The receptor type b.
	A; Reference number: S19021; MULD:92039815; PMID:1657766
	A; Accession: S19021
	A MOLECULE UPDE: IMANA A MOLECULE UPDE: IMANA A MOLECULE UPDE:
	A; Cross-references: EMBL:X57796; NID:g54848; PIDN:CAA40936.1; PID:g54849
	R;Bebo, B.F.
	Immunogenetics 39, 450-451, 1994
	A; Reference number: 154552; MUID:9424529; PMID:8188324
	A;Accession: 154532
	A.Status: translated from GB/EMBL/DDBJ A.Molegnie trace mbra
	A:Residues: 1-454 <res></res>
	A, Cross-references: GB: L26349; NID: 9430732; PIDN: AAA59361.1; PID: 9430733
	R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.
	MOI. Immunol. 30, 165-176, 1993 Noi. Immunol. 30, 165-176, 1993 Noi. Howard consensation and promoter function of the murine tumor necrosis factor
	A; ille: Geloult Urganization and Promotic Promotic A; Reference number: 157886; MUID:93156721; PMID:3381516

N

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A; Residues: 1-349 - SBL.>
A; Cross-references: UNIPROT: P34015; GB: X69198; NID: G456758; PIDN: CAA49137.1; PID: G457;
A; Cross-references: UNIPROT: P34015; GB: X69198; NID: G456758; PIDN: CAA49137.1; PID: G457;
A; Experimental source: strain India-1967, ssp. major, isolate Ind3
R; Kolykhalov, A.A.; Blinov, V.M.; Gytorov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F
submitted to the EMBL Data Library, April 1992
A; Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: variola virus
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D36858; S46888; S32385; S35987
C;Accession: D36858; S46889; S32385; S35987
Submitted to GenBank, November 1992
A;Accession: D36858
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N;Alternate names: B28R protein (COP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-348 < MAS>
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A;Molecule type: DNA
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A;Molecule type: DNA
A;Molecule type: DNA
A;Coss-references: GB:M76656; NID:g202100; PIDN:AAA40465.1; PID:g202102
C;Comment: This protein is one of two distantly related receptors for both TNF-alpha (ca
C;Comment: TNFR-2
A;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;213-235/Domain: transmembrane #status predicted <MEM>
F;226-454/Domain: intracellular #status predicted <INT>
F;54,151,202/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;84-126/Domain: NGF receptor repeat homology <NG2>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-204/Domain: NGF receptor repeat homology <NG4>
F;212-234/Domain: transmembrane #status predicted <MEM>
F;235-461/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.6%; Score 217.5; DB 1, 32.3%; Pred. No. 2.6e-09; ive 19; Mismatches 75,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 32.3 51; Conservative
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Best Local Similarity
Matches 49; Conserv
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Best Local S:
Matches 51
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A; Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449

1-349 <KOL>

5.

Gaps

13;

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Cjaccession: T28623
R; Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Av Rassung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Av A; Title: Potential virulence determinants in terminal regions of variola smallpox vir A; Reference number: Z20488; MUID:94088747; PMID:8264798
A; Recession: T28623
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4
A, Experimental source: strain Bangladesh 1975
C; Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                     71 DCPSPGQETVCEVCDKGTFTASQNHVRQCLSCKTCRKEMFQVEISPCKADMDTVCGCKKKN 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 KCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCS-T 105
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71
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                                                                      11 ISLVLLALLMGIHPSGVTGLVPSLGDREKRDNLCPQGKYAHPKNNSICCTKCHKGTYLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 KCKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGR
LLLLLLLLLLLLLLLLNL-----PLQVKFAMLELHSFKCPAGEY----WSKDVCCKNCSAGTFVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                         130 LYY-YDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
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20.0%; Score 201.5; DB 2
Best Local Similarity 35.5%; Pred. No. 3.4e-08;
Matches 44; Conservative 18; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein G2R - variola major virus
   21
   8
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A; Molecule type: mRNA
A; Residues: 1-455 < NOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: A36555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: A34899
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GZR protein - variola minor virus (strain Garcia-1966)

C;Species: variola minor virus

C;Species: variola minor virus

C;Species: variola minor virus

C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004

C;Accession: D72175

R;Abchcelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar submitted to GenBank, March 1998

A;Reference number: A72150

A;Reference mumber: A72150

A;Accession: D72175

A;Cross-references: UNIPROT:P34015; GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G58307

A;Esdidues: 1-349 < ASHC

A;Accession: C;Genetics:

A;Genetics:

A;Ge
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
BEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Residues: 31-168 <SHC>
A;Coss-references: EMBL:X69198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology F;32-6/Domain: NGF receptor repeat homology KNGF> F;68-109/Domain: NGF receptor repeat homology KNGF> F;68-109/Domain: NGF receptor repeat homology <NG3> F;110-151/Domain: NGF receptor repeat homology <NG3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 KCKDTEYKRHNLCCLSCPPGTYASRLCD-SKTNTQCTPCGSGTFTSRNNHLPACLSCNGR 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 20.0%; Score 201.5; DB 2; Length 349; l Similarity 35.5%; Pred. No. 3.4e-08; 44; Conservative 18; Mismatches 55; Indels 7
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                                                                                                                                                                                                                                                                                                                                                                                               A, Experimental source: strain India-1967, ssp. major
C, Genetics:
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Best Local Similarity
Matches 44; Conserva
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RESULT GQHUT1

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tumor necrosis factor receptor 1 precursor [validated] - human
N/Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
N/Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
                                                                                                                                                                Cispecies: Home sapiens (man)
Cipate: 30-Jun-1992 #text change 09-Jul-2004
Cipate: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
Cipate: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
Cipate: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
Cipate: 31, 219-224, 1992
A;Fuchs, P.; Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to chip A;Reference number: A38208; MuID:92250049; PMID:1315717
A;Reference number: A38208
A;Rolecule type: DNA
A;Residues: 1-455 <FUC>
A;Residues: 1-455 <FUC>
A;Residues: 1-455 <FUC>
A;Coss-references: UNIPROT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AJ
R;Loctecher; H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslaue
Cell 61, 351-359, 1990
A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept
A;Reference number: A34899; MUID:90235284; PMID:2158862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Note: part of this sequence, including the amino end of the mature protein, confirmed P. R; Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.. (edl 61, 361-370, 1990
A; Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. A; Reference number: A34900; MUID:90235285; PMID:2158863
A; Accession: A34900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Mesidues 1.455 «SCH»
A; Cross-references: GB: M33294; NID: 9339744; PIDN: AAA03210.1; PID: 9339745
A; Cross-references: GB: M3294; NID: 9339744; PIDN: AAA03210.1; PID: 9339745
R; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
R; Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; C
A; Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto:
A; Reference number: A36555; MUID: 91090841; PMID: 1702293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 30-38;41-53, 'X', 55-79, 'XX', 82-94, 'NK'; 'XX', 100-104;107-128;162-167, 'X', 169-20
A; Note: the purified protein, called tumor necrosis factor binding protein, is a soluble R; Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Nall. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A; Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re A; Reference number: A38281; MUID:91017509; PMID:2170974
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A; Residues: 1-455 <GRA>
A; Residues: 1-455 <GRA>
A; Cosserveferences: GR: M37764
A; Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R; Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
B; Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
B; Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
A; Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
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A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w
R;Kemper, O.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-13 «KEM»
A;Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Bur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc
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A;Title: Cloning and partial characterization of the promoter for the human p55 tumor ne
A;Reference number: JT0758; MUID:94085779; PMID:8262379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-455 < LOB>
A; Cross-references: GB:MS9286; GB:M33480; NID:g339753; PIDN:AAA36753.1; PID:g339754
A; Experimental source: placenta
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A;Cross-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
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C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C,Accession: S12783; S08036
E;Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A,Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphoc A,Reference number: S12783; MUID:90214614; PMID:2157591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT:P15725; EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:9578
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Reywords: growth factor receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-271/Product: OX40 antigen #status predicted <MAT>
F;211-235/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-461 <SUT>
A;Cross-references: UNIPROT:PS0555; GB:U19994; NID:g1141752; PIDN:AAC48499.1; PID:g11
                                                                                                                                                              tumor necrosis factor receptor p55 precursor - pig
C;Species: Sus scrofa domestic pig)
C;Date: 29-NOV-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: JG4302; PC4093
R;Suter, B.; Pauli, U.
R;Suter, B.; Pauli, U.
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.
A;Reference number: JG4302; MUID:96011645; PMID:7590278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 DCLGPGLDTDCRECDNGTFTASENHLTQCLSCSKCRSEMSQVEISPCTVDRDTVCGCRKN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTC--DKDQEMVADCSATSDRKCQCRTG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>
F;44-82/Domain: NGF receptor repeat homology <NGI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 LLLLLLLLLLLLL-PLQVKFAML-----ELHSFKCPAGEY---WSKDVCCKNCSAGTFVKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F.14-82/Domain: NGF receptor repeat homology <NGI>
F.34-126/Domain: NGF receptor repeat homology <NGF>
F.341-231/Domain: NGF receptor repeat homology <NGF>
F.311-231/Domain: transmembrane #status predicted <TMM>
F.361-447/Domain: signal transduction #status predicted <SIT>
F.361-447/Domain: aignal transduction #status predicted covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 LY -- YYDPKFPESCRPCTKCPOGIPVLOECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 QYRKYWSETLFQ-CLNCSLCPNG-TVQLPCLEKQDTICN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OX40 antigen precursor - rat
N;Alternate names: nerve growth factor receptor homolog
C;Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carbuing 19.9%; Score 200.5; DB 2; nn 8%; Pred, No. 4.9e-08; 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: kidney cell line 15
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Matches 51; Conservative
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Best Local Similarity
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A; Residues: 1-271 < MAL>
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A; Residues: 41-53, X',55-144, X',146-150, X',152-186, X',188-201 < KAJ>
A; Residues: 41-53, X',55-144, X',146-150, X',152-186, X',188-201 < KAJ>
A; Experimental source: urine
C; Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and C; Genetics:
A; Genetics: A; Fig. 125913; OMIM:191190
A; Map position: 12p13.2-12p13.2
A; Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C; Superfamily: tumor necrosis factor receptor; transmembrane protein
C; Keywords: duplication; 91ycoprotein; receptor; transmembrane protein
C; Keywords: duplication; 91ycoprotein; receptor 1 #status predicted < SIG>
F; 12-10 Domain: signal sequence #status predicted < SIG>
F; 22-455/Product: tumor necrosis factor receptor 1 #status predicted < MAT>
F; 12-10/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status
F; 44-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor)
F; 44-126/Domain: NGF receptor repeat homology < NG3>
F; 12-167/Domain: NGF receptor repeat homology < NG3>
F; 16-196/Domain: NGF receptor repeat homology < NG3>
F; 16-196/Domain: intracellular #status predicted < MEM>
F; 18-1-201/Product: transmembrane #status predicted < MEM>
F; 18-1-201/Product repeat homology < NG3>
F; 18-196/Domain: intracellular #status predicted < NEM>
F; 18-1-196/Domain: intracellular #status predicted < NEM>
F; 21-2-234/Domain: intracellular #status predicted < NEM>
F; 24,145,151/Binding site: carbohydrate (Asn) (covalent)
A;Reference number: A60231; MUID:90292116; PMID:2113477
A;Accession: A60231
A;Accession: A60231
A;Accession: A60231
A;Accession: A60231
A;Redidues: Protein
A;Redidues: A1-43, X', 45-53, X', 55-57
A;Redidues: T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; LeProc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis factotienes.
A;Reference number: A38258; MUID:91062364; PMID:2174164
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, Molecule 1, M
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A; Residues: 41-45 < ENG>
A; Residues: 41-45 < ENG>
A; Experimental source and urine
B; Kajihara, J; Asada, A.; Kirihara, S.; Kato, K.
B; Kajihara, J; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A; Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A; Reference number: JC2404; MUID:95128033; PMID:7765720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 30.6
Matches 49; Conservative
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71

Gaps

15;

Indels

Length 461;

<u>ب</u>

Gaps

40;

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Best Local Similarity 34.74
Matches 50, Conservative
                                                  A; Molecule type: mRNA
A; Residues: 1-427 <JOH>
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A;Cross-references:
                                                                                                                                                                             Accession: A60204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nerve growth factor receptor precursor, low affinity [validated] - human N; Alternate names: NGF receptor C; Species: Homo sapiens (man) C; Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text_change 09-Jul-2004 C; Accession: A25218; A60204; S21689; I57638 R; Johnson, D.; Lanahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fas antigen in the rat live
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                              111 RQDSSHKLGVDCVPCPPGHFSPGSNQACKPWTNCTLSGKQIRHPASNSLDTVCED----R 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SAGTFVKAPCEIPHTQGQCEKCHPGT----FTEKDNYLDACILCSTCDKDQ--EMVADCS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 OPGERKVKDCT---TSGGAPTCHPCTEGEEYTDRKHYSDKCRRCAFCDEGHGLEVETNCT 116
                                                                                                    -HTRDTVCHPCEPGFYNEAVNY-DTCKQCTQCNHRSGSELKQNCTPTEDTVCQCRPGTQP 110
                                                                                                                                         ---YYDPKFPESCRPCTKCP-QGIPVLQECNSTANTVCSSSVSRR 172
                                                                    PHTQGQ-CEKCHPGTFTEKDNYLDACILCSTCD--KDQEMVADCSATSDRKCQCRTGLY- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                                 52
                                                                                                                                                                                                                                                                                                                                                        C;Species: Rattus norvegicus (Norway rat)
C;bate: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;bate: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: 022345; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Ress. Commun. 189, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated from of Fas antigen in A;Reference number: JC2395; MUID:94128114; PMID:7507668
                  17 IMRRILLILLILLILLILLINDPLQVK-----FAMLELH-----SFKCPAGEYWSKDVCCKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 ATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGI-PVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 188; DB 2; 29.3%; Pred. No. 3.3e-07; ive 25; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Conservative
                                                                                                                                                                                                                                                                                                                                         Fas antigen precursor - rat
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SLLATLLW 174
                                                                                                                                                                                                                S--ASVAW 178
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Matches 51; Conserv
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A;Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AABS9544.1; PID:g189205 R;Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schatteman, G.; Thompson, S.; Grob, P.; N. Neurochem. 48, 225-232, 1987.
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth facton A;Reference number: A60204; MUID:87085574; PMID:3025363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A; Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A; Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, XX', 54-56 <MAR>
A; Residues: Borce: melanoma cell line A875
A; Note: this sequence has been corrected by a note added in proof to follow the nucleotic R; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
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A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
A; Vissavajjhala, P.; Lin-Goerke, J.J.; 
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A;Status: preliminary
A;Molecule type: protein
B;Rehgal, A.; Patil, N.; Chao, M.
Mol. Call. Biol. 8, 3160-3167, 1988
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor § A;Reference number: I57638; MuID:89096903; PMID:2850481
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C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoms or C;Comment: The cysteine-rich region of the extracellular domain may form part or all of a C;Comment: This protein is thought to form a high-affinity receptor when it associates w. C;Comment: This receptor undergoes both N- and O-linked glycosylation.
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C; Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C; Superfamily: nerve growth factor receptor; MGF receptor repeat homology
C; Keywords: duplication; glycoprotein, predicted <81G>
F; 1-29 Domain: signal sequence #status predicted <81G>
F; 29-427/Product: nerve growth factor receptor #status experimental <MAT>
F; 29-427/Product: nerve growth factor receptor #status predicted <8XT>
F; 29-250/Domain: extracellular #status predicted <8XT>
F; 29-256/Domain: NGF receptor repeat homology <NG2>
F; 67-108/Domain: NGF receptor repeat homology <NG3>
F; 149-189/Domain: NGF receptor repeat homology <NG3>
F; 149-189/Domain: NGF receptor repeat homology <NG4>
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F:551-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding Bite: carbohydrate (Asn) (covalent) #status predicted
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A;Title: Expression and structure of the human NGF receptor A;Reference number: A25218; MUID:87051725; PMID:3022937
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A;Molecule type: DNA
A;Residues: 1-22 <RES>
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11; Mismatches
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receptor family, below

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C;Date: 17.Jan-1992 #sequence_revision 17.Jan-1992 #text_change 09.Jul-2004
C;Accession: A40036; S24543; A38142
R;ItOh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hatell 66, 233-243, 1991
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can makReference number: A40036; MUID:91309137; PMID:1713127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P25445; GB:M67454; NID:g182409; PIDN:AAA63174.1; PID:g182
R;Krammer, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fil-21/Domain: signal sequence #status predicted <SIG>
Fil-21/Domain: sxtracellular cysteine-rich, ligand-binding #status predicted <ECL>
Fi322-350/Domain: transmembrane #status predicted <TWM>
Fi310-475/Domain: death domain #status predicted <TWM>
Fi410-475/Domain: death domain #status predicted <CL>
Fi410-475/Domain: conserved cytoplasmic #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 KSTLRECSPCPDGTFTKHENGIERCHPCRKPCELPMIEKTHCTALTDRECTCLSGTF--- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 PHIQGQCEKCHPGTFTEKDNYLDACILC-SICDKDQEMVADCSAISDRKCQCRIGLYYYD 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 CSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRR 172
                                                                                                                                                                                                                                                                                                                            C;Species: Gallus gallus (chicken)
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: JC7705
R;Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
A;Title: Conservation of death receptor-6 in avian and piscine vertebrates.
A;Reference number: JC7705; MUID:21308433; PMID:11414698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LLLLLLLLLLLLLLVVKFAMLELHSFKCPAGEY-----WSKDVCCKNCSAGTFVKAPCEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.9%; Score 180.5; DB 2; Length 651; 29.8%; Pred. No. 1.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:098SM6; GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor re
tresia, activates a cell death and/or survival signaling cascade.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  apopiosis-mediating surface antigen Fas precursor - human N;Alternate names: surface antigen APO-1 C;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: X63717; NID: 928741; PID: 928742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, February 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27; Mismatches
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                                                                                                                                                                                                                                                                                                 death receptor-6 - chicken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-651 <BRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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A,Molecule type: mRNA
A,Residues: 1-335 <ITO>
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A; Residues: 1-335 < KRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Keywords: ovary
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A46484

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A90ptosis-mediating membrane-associated polypeptide Fas - mouse
C;Species Mas macaulus (house mouse)
C;Date: 18-Unn-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Date: 18-Unn-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A46484; A47254
R;Watanabe-Pukunaga, K: Brannan, C.I.; Itoh, N.; Yonehara, S.; Copeland, N.G.; Jenkins, J. Immunol. 148, 1274-1279, 1992
A;Pitle: The CDNA structure, expression, and chromosomal assignment of the mouse Fas ant A;Reference number: A46484; MUID:92148151; PMID:1371136
A;Reference number: A46484
A;Reference number: A46484; MUID:92148151; PMID:137136
A;Residues: 1-377 cwarz
A;Cross-references: UNIPROT:P25446; GB:M83649; NID:g193225; PIDN:AAA37593.1; PID:g193226
A;Residues: 1-377 cwarz
A;Residues: 1-377 cwarz
A;Residues: 1-377 cwarz
A;Residues: 1-377 cwarz
A;Residues: 1-377 cwarz
A;Residues: 1-377 cwarz
A;Reference mumber: A47254; MUID:93189576; PMID:7680478
A;Reference number: A47254; MUID:93189576; PMID:7680478
A;Residues: 1-96 cwalp.
A;Residues: 1-96 cwalp.
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C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 137383,
B;Cascino, I.; Fiucci, G.; Papoff, G.; Ruberti, G.
J. Immunol. 154, 2706-2713, 1995
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are A;Reference number: 137383; MUID:95181785; PMID:7533181
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C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 PCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVADCSATSDRKCQCRT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 CCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVAD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 LPLVLAGSQLRVHTQGTNSISESLKLRRRVHETDKNCSEGLYQGGPFCCOPCOPGKKKVE 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32 LPLQVKFAMLELH----SFK-----CPAGEYWSKDVCCKNCSAGTFVKA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.1%; Score 182; DB 2; Length 314; ilarity 31.6%; Pred. No. 9.1e-07; Conservative 20; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.2%; Score 183; DB 2; Length 327; larity 27.6%; Pred. No. 7.8e-07; Conservative 23; Mismatches 69; Indels
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FAS soluble protein - human
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Matches 37; Conserva
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A; Residues: 1-314 <RES>
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Best Local S
Matches 45
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A; Residues: 1-416 < LLAR>
A; Cross-references: UNIRDOT: P18519
A; Cross-references: UNIRDOT: P18519
A; Experimental source: embryonic chick brain
R; Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Bot. 137, 287-304, 1990
A; Title: Structure and developmental expression of the chicken NGF receptor.
A; Reference number: A60504; MUID: 90152140; PMID: 2154393
A; Accession: A60504
A; Reternce number: A60504; MUID: 90152140; PMID: 2154393
A; Accession: A60504
A; Reternce number: A60504; MUID: 90152140; PMID: 2154393
A; Accession: A60504
A; Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 < HEU>
C; Comment: This receptor is found on sensory and sympathatic neurons, on neuroblastoms
C; Comment: This procein is thought to form a high-affinity receptor when it associates w
C; Comment: This procein is thought to form a high-affinity receptor when it associates w
C; Comment: This protein is thought to form a high-affinity receptor when it associates w
C; Comment: This protein is ground afficient in production of the extracellulal affinity receptor repeat homology of C; Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; F; 1-20/Domain: signal sequence #status predicted & SIG>
F; 21-416/Product: nerve growth factor receptor #status predicted & SIG>
F; 21-230/Domain: NGF receptor repeat homology < NG2>
F; 24-57/Domain: NGF receptor repeat homology < NG3>
F; 101-139/Domain: NGF receptor repeat homology < NG3>
F; 101-139/Domain: NGF receptor repeat homology < NG3>
R;Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; Rich J. Biol. Chem. 267, 10709-10715, 1992
A;Title: Purification and molecular cloning of the APO-1 cell surface antigen, a member A;Reference number: A38142; MUID:92268122; PMID:1375228
A;Accession: A38142
A;Accession: A38142
A;Eatus: preliminary; not compared with conceptual translation
A;Residues: 1-134, O', 136-335 coBH>
A;Residues: 1-134, O', 136-335 coBH>
A;Residues: 1-134, O', 136-315 coBH>
A;Note: sequence extracted from NCBI backbone (NCBIP:103810)
A;Note: in NCBI backbone the source is designated as mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NiAlternate names: NGF receptor
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JN0006; A60504
R;Large, T.H.; Weskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reic
Astrile: Structure and developmental expression of the nerve growth factor receptor in the A;Reference number: JN0006; MUID:90166579; PMID:2560385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 10q24.1-10q24.1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homold
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCKNCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQ--EMVAD 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSAS 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JN0006
nerve growth factor receptor, low affinity precursor - chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Keywords: apoptosis; surface antigen; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <51G>
F;12-128/Domain: NGF receptor repeat homology <NG4>
F;174-190/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: GDB:APT1
A,Crose-references: GDB:132671; OMIM:134637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: JN0006
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

September 8, 2005, 23:31:32; Search time 672.857 Seconds (without alignments) 136.989 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-622-407-10 1008 1 MFGFFCSLVSSLSRWFLWRR......ANTVCSSSVSRRSASVAWPI 180

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	-	Description	Q9er62 mus musculu	Q9er63 mus musculu		Q7t3m7 gallus gall	Q7t3m8 gallus gall	_	Q800k8 paralichthy	Q9df34 brachydanio	Q6dj81 xenopus tro		Q6glz4 xenopus lae		Q95185 felis silve	Q95nd3 felis silve	Q76b98 xenopus lae	O57119 cowpox viru	Q6qhf0 mus musculu	Q6qhfl mus musculu		097530 canis famil	O57118 cowpox viru	O57120 cowpox viru	O57103 monkeypox v	_	-	_	057102 monkeypox v	-	O57305 cowpox viru	O57121 cowpox viru	P51867 bos taurus
SUMMAKIES		ΩI	TR22 MOUSE	TR23 MOUSE	TR26_MOUSE	Q7T3M7	Q7T3M8	Q9DFV0	Q800K8	Q9DF34	Q6DJ81	Q76B99	Q6GLZ4	Q678B7	Q95185	Q95ND3	076898	057119	Оебньо	Q6QHF1	TRIA MOUSE	097530	057118	057120	057103	057108	057277	057101	057102	057291	057305		TNR6_BOVIN
		B	7	-1	-	N	α	~	~	~	7	N	~	~	~	7	~	~	~	N	Н	7	N	N	7	7	~	7	N	N	~	0	П
		Match Length DB	198	176	204	225	410	438	395	357	321	328	328	289	189	446	328	347	440	440	454	189	360	326	348	348	348	349	349	349	.349	351	323
۵	Query	Match	94.8	69.8	29.7	28.4	28.4	27.3	27.1	25.7	24.8	24.7	24.6	23.8	23.7	23.1	23.0	21.9	21.6	21.6	21.6	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.4	21.3
		Score	926	705	299	286.5	286.5	275.5	273.5	. 259	249.5	249	248	239.5	239	233	232	221	217.5	217.5	217.5	216	216	215.5	215.5	215.5	215.5	215.5	215.5	215.5	215.5	215.5	215
	Result	No.	-	8	m	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	59	30	31

Q6ghf2 mus spretus O6wb14 callithrix O57122 cowpox viru O73559 cowpox viru O57099 monkeypox v O7736 sus scrofa O77736 sus scrofa O9x860 oryctolagus O9x829 oryctolagus O5x115 cowpox viru Q8wya7 camelpox viru Q8wya7 camelpox viru O8y100 monkeypox v
06CHF2 06WB14 057122 CRWB COWPX 057129 077224 TRN6 PIG 09XS0 057715 057715 057715 057710
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444 444 444 444 444 444 444 444 444 44
200.9 200.9 200.9 200.9 200.9 200.9
214.5 213.5 213.5 213.5 211.5 211.5 211.5 211.5 210.5 200.5
U U U U U U U U U U U U U U U U U U U

ALIGNMENTS

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Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchioni L., McKenzie L., Miki H.,
Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pescle G.,
B. Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Sample C.A., Setcou M., Shimada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wanner L., Wahlestedt C., Wang Y., Watnabe Y., Walls C.,
Wilming L.G., Wynshaw-Boris A., Vanagisawa M., Yang I., Yang I.,
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Komno H., Nakamura M., Sakzume N., Sato K.,
A Hirozane-Kishikawa T., Komno H., Nakamura M., Sakzume N., Sato K.,
A Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Lander E.S., Rogers J.,
Miyazaki A., Mara M., Materston R., Lander E.S., Rogers J.,
Miyazaki A., Manulshi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Miyazaki A., Manulshi A., Woshino W., Waterston R., Lander E.S., Rogers J.,
Miyazaki A., Manulshi A., Woshino W., Waterston R., Lander E.S., Rogers J.,
Miyazaki A., Manulshi A., Woshino W., Waterston R., Lander E.S., Rogers J.,
Miyazaki A., Manulshi A., Woshino W., Waterston R., Lander E.S., Rogers J.,
Miyazuki A., Manulshi A., Woshino W., Materston R., Lander E.S., Rogers J.,
Miyaruka M., Mature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its meeb by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9ER62-2; Sequence=VSP_007648;
ISSUE SPECIFICITY: Ubiquitous.
SIMILARITY: Contains 3 TNFR-Cys repeats.
CAUTION: Ref.1 (CAC27353) sequence differs from that shown due to
erroneous gane model prediction.
CAUTION: Ref.1 (CAC16406) sequence differs from that shown due to
a frameshift in position 38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis. Protects cells against TRAIL mediated apoptosis possibly through ligand competition. Cannot induce the NF-kappa-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. Lacks cytoplasmic death domain and hence is not capable of inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alternative splicing; Glycoprotein; Receptor; Repeat; Signal-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
TNFR-Cys 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pathway.

BUGGELLUAR LOCATION: Type II membrane protein (isoform 1);
secreted (isoform 2) (Potential).

ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; Q92956; LDM.
MGD; MGI:1930270; Thfrsf22.
MGD; MGI:1930270; Thfrsf22.
GO; GO:0016621; C:integral to membrane; NAS.
GO; GO:0004872; F:receptor activity; IDA.
GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
GO; GO:0045569; F:TRAIL binding; IDA.
GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.
InterPro; IPR001368; TNFR.c6.
Pfam; PF00020; TNFR.c6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event-Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=1;
IsoId=09ER62-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AJ278265; CAC16406.1; ALT_FRAME.
EMBL, AJ276505; CAC27353.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AY046551; AAL05073.1; -. AK012838; BAB28502.2; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00652; TNFR NGFR 1; 3. PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AY165626; AAN87806.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AY165627; AAN87807.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
41
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61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPRNRLFLLLSPLSVLIVSVVVFRIIRR -> RRSASVAWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLBLHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERG3: QBVHCO;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 44, Last sequence update)
59-FEB-2004 (Rel. 44, Last sequence update)
5-JUL-2004 (Rel. 44, Last sequence update)
Tumor necrosis factor receptor superfamily member 23 precursor (Tumor necrosis factor receptor p60 homolog 1) (TNF receptor family member SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).
Name=Thfrsf23; Synonyms=Dctrailr1, Thfrh1, Thfrsflal1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=1295V; TSSUB-Embryonic stem cells; MEDLINE=2051929; PubMed=11063728; DOI=10.1093/hmg/9.18.2691; Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R., Lane N., Reik W., Walter J.; Ranck O., Reinhardt R., Ranck W., Raik W., Walter J.; Ranck O., Reinhardt R., Ranck M., Raiter J.; Ranck M., Raiter J.; Ranck M., Raiter J.; Ranck M., Raiter J., Ranck M., Raiter J., Ranck M., Raiter J., Ranck M., Raiter J., Ranck M., Raiter J., Ranck M., Raiter J., Ranck M., Raiter J., Raiter J., Raiter J., Ranck M., Raiter J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=12466268; DOI=10.1074/jbc.M210783200; Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Burkly L.C., Tschopp J., Zheng T.S.; Mofmann K., Van Vlijmen H., Hsu Y.-M., Burkly L.C., Tschopp J., Zheng T.S.; Indementification of a new murtine tumor necrosis factor receptor locus indementation two novel murine receptors for tumor necrosis factor related apoptosis-inducing ligand (TRAIL).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE MODELING OF 52-160.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                    By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. . .) (Potential).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRKCOCRTGLYYYDPKFPESCRPCTKCPQGIPVLOECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 DRKCÓCRIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. No. 5.3e-75; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
TNFR-Cys 2.
TNFR-Cys 3.
By similarity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.8%; Score 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3est Local Similarity 100.0
4atches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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84
48
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1106
1126
1144
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=12465268; DOI=10.1074/jbc.M210783200;
PubMed=12465268; DOI=10.1074/jbc.M210783200;
Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,
Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,
Burkly L.C., Tschopp J., Zheng T.S.;
"Identification of a new murine tumor necrosis factor receptor locus
that contains two novel murine receptors for tumor necrosis factor-
related apoptosis-inducing ligand (TRAIL).";
J Biol. Chem. 278:5444-5454 (2003).
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND 3D-STRUCTURE MODELING OF
                                                                                                                10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 26 precursor (TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 278:5444-5454(2003).
-!- SUBCELUIAR LOCATION: Type I membrane protein (Potential).
-!- TISSUE SPECIFICITY: Expressed in thymus and spleen. Detectable levels in lung.
-!- SIMILARITY: Contains 3 TNPR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
TNFR-Cys 3.
Cys-rich.
By similarity.
N-linked (GlCNAC. . . ) (Potential).
                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor necrosis factor receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 superfamily member 26.
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MUDIO MGI-SE51928; TRIFREFER THE TREFER THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -linked (GlcNAc. . .) (Pot A35C5177F178C3DD CRC64;
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41.3%; Pred. No. 3.8e-18;
iive 24; Mismatches 56;
                                            204 AA
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                                                                                                                                                                                         receptor homolog 3).
Name=Tnfrsf26; Synonyms=Tnfrh3;
                                                                                           10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequ
05-JUL-2004 (Rel. 44, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY165628; AAN87808.1; -.
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22708 MW;
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                                            STANDARD;
                                                                                                                                                                                                                      Name=Tnfrsf26; Synon
Mus musculus (Mouse)
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les 59; Conserv
                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                               MOUSE
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Matches
                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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Removed in mature form (Potential).
GPI-anchor amidated cysteine (Potential).
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                                       -linked (GlCNAc. . .) (Potential). EE30D617F49DDB7D CRC64;
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GO; GO:0005515; F:protein binding; IPI.

GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.

InterPro; IPRO01368; TNFR_G6.

Ffam; PF00020; TNFR_G6; 3.

SMART; SM00208; TNFR_G6; 3.

SMART; SS0052; TNFR_NGFR_1; 3.

PROSITE; PS50050; TNFR_NGFR_2; 2.

Glycoprotein; GPI-annopr; Lipoprotein; Receptor; Repeat; Signal.

SIGNAL.
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                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
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TNFR-Cys 3.
Biol. Chem. 278:5444-5454(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AJ278264; CAC16405.1; ---
EMBL; AJ276505; CAC27352.1; ---
EMBL; AY165625; AAN87805.1; ---
EMBL; AY046550; AAL05072.1; ---
HSSP; Q92956; IJMA.
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131
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Name=tnfrsfa;
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                                                                                                                                                                                                                                                                                                                                                                                               SEQÜENCE
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9DFV0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9DFV0
                                                                                  Gallus
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                                                         83 EKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCR 142
                                                                    62 APCDSEHFIDHKNRESECFPCSVCRDDQEEVAKCSRTADRVCQCKQGTYCDSENCLERCH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKF 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RRLLLLLLLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 RAVGLLILVTLLTVP----GSXAEV----CGEGEYLXEDICCMLCPAGTYVAQHCRIPHS 55
                       4 LRLLLLLGLLLRV--AVCSVNTTTLCKIGEFKHENLCCLQCSAGTYLRNPCQENHNKSEC 61
                                                                                                                                                                                                                                                                                                                                                                      Bridgham J.T., Johnson A.L.;
"Alternatively spliced variants of Gallus gallus TNFRSF23 are
expressed in the ovary and differentially regulated by cell signaling
         LILLILLILLINDPLOVKFAMLELHSFK-CPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQC
                                                                                                                                                                                                                                                              member 23 variant 2.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28.4%; Score 286.5; DB 2; Length 225;
39.6%; Pred. No. 5e-17;
ive 26; Mismatches 53; Indels 11; Gaps
                                                                                                                                                                                                                          01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Death domain-containing tumor necrosis factor receptor superfamily
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 AA; 24697 MW; 59FC9C0AE4530630 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP, 014763, 1DU3.

GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
InterPro; IPR001368; TNFR_c6.
INTERPROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS01186; BGF_2, UNKNOWN_1.
PROSITE; PS01186; BGF_2, INTER_NGFR_1; 1.
PROSITE; PS00050; TNFR_NGFR_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               410 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 CEICQRCTETCPEGREIVQICNATMDLGC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PESCRPCTK-CPQGIPVLQECNSTANTVC 165
                                                                                                       143 PCTKCPQGIPVLQECNSTANTVC 165
                                                                                                                     122 TCSSCPDG-RVVRKCNATMDTVC 143
                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
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01-OCT-2003 (TrEMBLrel. 25, Created)
                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                           pathways.";
Biol. Reprod. 70:972-979(2004)
EMBL; AY251409; AAP41834.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 39.63 S9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                            PubMed=14645108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Q7T3M8
ID Q7T3I
AC Q7T3I
DT 01-O
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79 QGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKF 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 RRILLILLILLILLILLINLPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHT 78
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRA-2004 (TrEMBLrel. 26, Last annotation update)
Death domain-containing tumor necrosis factor receptor superfamily
member 23 variant 1 (Fragment).
Gallus gallus (Chiken).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bobe J., Goetz F.W.;
Molecular cloning and expression of a TNF receptor and two TNF ligands in the fish ovary.";
Comp. Biochem. Physiol. B. Comp. Biochem. 129:475-481(2001).
EMBL; AF250042; AAG24365.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 410;
                                                                                                                                                                                                                                                                                                                                                                Bridgham J.T., Johnson A.L.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY251408; AAP41833.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46194 MW; 4BFC7C7016C2BA60 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Ovarian TNF receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO: 00.005515; F: protein binding; IEA.
GO: 00.004872; F: protein binding; IEA.
GO: 00.004872; F: preceptor activity; IEA.
GO: 00.001165; P: signal transduction; IEA.
InterPro: IPR001485; Death.
InterPro: IPR001489; Death.
InterPro: IPR001629; BGF like.
InterPro: IPR00159; BGF like.
InterPro: IPR00159; BGF like.
InterPro: IPR001589; TWFR_C6.
Pfam; PF0020; TWFR_C6; 3.
SMART; SM00209; TWFR_C6; 3.
SMART; SM00209; TWFR, 3.
PROSITE; PS00198; 4FE45; FERREDOXIN; UNKNOWN_I.
PROSITE; PS00198; GGF 2; UNKNOWN_I.
PROSITE; PS01186; EGF 2; UNKNOWN_I.
PROSITE; PS01186; EGF 2; UNKNOWN_I.
PROSITE; PS01186; EGF 2; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.4%; Score 286.5; DB 2; 39.6%; Pred. No. 8.7e-17; tive 26; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 438 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 PESCRPCTK-CPQGIPVLQECNSTANTVC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 CEICQRCTETCPEGREIVQICNATMDLGC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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66 GTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQ 125
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                                                                                                                                                                                                                                               9 RLLVLLLSSTGVFPQSRIDFGRRTQRDILCSDNQYLNGNNCCLNCPAGTHVKSHCSKSGE 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20394298; PubMed=10934476; DOI=10.1038/35019592;
Long Q., Huang H., Shafizadeh B., Liu N., Lin S.;
"Stimulation of Erythropoiesis by inhibiting a new hematopoietic death receptor in transgenic zebrafish.";
Nat. Cell Biol. 2:549-552(2000).
EMBL; AF302789; AAG21396.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 RILLILLILLILLILLINL-------PLQVKFAMLELHSFKCPAG-EYWSKDVCCKNCSA
                                                                                                                                                                                                                      20 RILLILLILLILLINDP-LQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; (vanio rerio).
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                            | |: |: || : : : | || || || EVCKKCSKCEKDVIAVVFPI 178
                                                                                                                                                                                                                                                                                                                                                                                                 139 ESCRPCTKCPQGIPVLQECNSTANTVC-----SSSVSRRSASVAWPI 180
                                                                                                                                   Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 259; DB 2; Length 357; 32.9%; Pred. No. 1.8e-14;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;
                                                                                     395 AA; 44304 MW; 8D685A9F74710AE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                            Query Match 27.1%; Score 273.5; DB 2; Best Local Similarity 34.1%; Pred. No. 1.1e-15; Matches 58; Conservative 28; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; Q92956; iJMA.
ZPIN; ZDB-GENE-030826-5; hdr.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:00016515; P:signal transduction; IEA.
InterPro; IPR004088; Death.
InterPro; IPR001368; TWFR_GG.
Fam; PF00531; Death; 1.
Ffam; PF00531; Death; 1.
Ffam; PF00520; TWFR_GG; 3.
PROSITE; PS000620; TWFR_NGFR_1; 3.
PROSITE; PS000652; TWFR_NGFR_1; 3.
PROSITE; PS000652; TWFR_NGFR_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Mismatches
PROSITE; PSS0017; DEATH DOMAIN; 1.
PROSITE; PS00652; TNFR NGFR 1; UNKNOWN 2.
PROSITE; PS50050; TNFR NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Conservative
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Matches 56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Death receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
                                                                       Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                               129
                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 LELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDAC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 ILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNST 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98 LOCSQCHRDQTVVAECTSTSNTKCDCKFGTFCLPDEPCEVCKKCTKCKADEEEVSGCTPT 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Paralichthys olivaceus (Japanese flounder).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Meopterygii; Teleostei; Buteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Pleuronectoidei; Paralichthyidae; Paralichthys.
                                                                                                                                                                                                                                                                                                                                                                                                                          27.3%; Score 275.5; DB 2; Length 438; 39.2%; Pred. No. 8.3e-16; ive 18; Mismatches 51; Indels 7
                                                                                                                                                                                                                                                                                                                                                                              438 AA; 49103 MW; B7E5312BE6E80B04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                  ZETI, ZDB-CENE-010802-1; tnfrsfa.
ZETI; ZDB-CENE-010802-1; tnfrsfa.
GO; GO:0004915; P:protein binding; IEA.
GO; GO:0004915; P:protein binding; IEA.
GO; GO:000165; P:signal transduction; IEA.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR001345; CytC heme_BS.
InterPro; IPR011029; Death like.
InterPro; IPR011029; DEATH like.
InterPro; IPR001368; TNFR_G6.
Pfam; PF00020; TNFR_C6; 2.
SMART; SM00208; TNFR, 6; 2.
SMART; SM00208; TNFR, 3.
PROSITE; PS00190; CYTCCHROME C; UNKNOWN_1.
PROSITE; PS00050; TNFR, MGFR_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO: 0005676; F: nucleic acid binding; IEA. GO; GO: 0005515; F: protein binding; IEA. GO; GO: 0004872; F: receptor activity; IEA. GO; GO: 000165; P: signal transduction; IEA. InterPro; IPR010488; Death. InterPro; IPR010489; DEATH. like. InterPro; IPR0101368; TWFR. GC. InterPro; IPR01189; ZAF_GCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         395 AA
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EMBL; AB080946; BAC65225.1; -.
HSSP; O14763; 1DU3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR c6; 2.
SMART; SM00208; TNFR; 3.
SMART; SM00343; ZnF_C2HC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SNTKC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8255;
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                                                                                                                                                                                                                                                                                                                                                              Receptor.
SEQUENCE
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Q800K8

RESULT CRESULT
Matches

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Name=xDR-M1:
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MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MELAUSPER R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Menstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Mhiting M., Madan J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Morriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Generation and initial analysis of more than 15,000 full-length human
and mouse C.DNA sequences."
                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
CRIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSAS 175
                            24.8%; Score 249.5; DB 2; Length 321; larity 33.3%; Pred. No. 1.1e-13; Conservative 23; Mismatches 64; Indels 31.
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A Klein S., Gerhard D.S.;

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Klein S., Gerhard D.S.;

Klein GO: 6000515; F: Protein binding; IEA.

GO; GO: 60006872; F: Protein binding; IEA.

GO; GO: 600165; F: Protein binding; IEA.

A InterPro; IPR001450; 4Fe4S ferredoxin.

R InterPro; IPR001369; TWFR.—G.

R Ffam; PF00531; Death; 1.

R Ffam; PF00531; Death; 1.

R Ffam; PF00050; TWFR.—G.

R SMART; SM00005; TWFR. 2.
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                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                       25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus
NCBI_TaxID=8364;
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Best Local Similarity
Matches 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                    Q6DJ81
Q6DJ81;
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64 SAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATSDR 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 MVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTK-CPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 EVRSCTATONAECRCKKGTYCPMDHPCEVCLTCTESCPPGQELHLPCNSTSDSHCGPAES 157
                                                                                                                                                                                       41 PAGTFVEKPCTKPDTIGECSSCHTGSTYSEGPTGLDHCLTCLRCRDDQEEVRPCTATONA 100
                                                            8 FFC-----YQEGNIRCLRC 40
                                                                                                                                                                                                                                                      123 KCQCRIGLYYYDPKFPESCRPCT-KCPQGIPVLQECNSTANTVCSSSVSRRSASVAW 178
                                                                                                                                                                                                                                                                                               :|:|: | | : : | : : | : : | ERRCRYGTYCPIDHPCEVCLICTEKCPPGQELQFPCNSTSDSQCGPAES--GSWIVW 155
PFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCCKNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
PubMed-14668140; DOI=10.1074/jbc.M306217200;
Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
"Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.7%; Score 249; DB 2; 38.3%; Pred. No. 1.2e-13; tive 22; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEAM; PF00531; Death; 1.
PFAM; PF00231; DEATH; 1.
SMART; SM00020; DEATH; 1.
PROSITE; PS00198; 4FF4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00107; DEATH_DOWAN, 1.
PROSITE; PS00622; TWRR NGFR 1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      differential mechanisms...;
J. Biol. Chem. 279:7629-7635(2004).

EMB1, AB11146; BAD11770.1;
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0001455; P:signal transduction; IEA.
InterPro; IPR001459; Pfe45_ferredoxin.
InterPro; IPR011029; DEATH like.
InterPro; IPR011029; DEATH like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 RRSASVAW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 GSLKTWIW 165
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ses 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Death receptor-M1.
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RESULT

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Gaps

31;

38 YQAGNIRCLACPAGTYVEEPCTTRDTKGECIPCHPGSTYSEGPTGLDHCLSCSRCRDDQE 97

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**REDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

**Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**RIALINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

**Altachul S.F., Zeeberg B., Wagner L., Schaefer C.F., Bhat N.K.,

**Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**Altachul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

**Altachul S.F., Zeeberg B., Bonaldo M.F., Carninci P., Wilsie F.,

**Altachul M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C.,

**Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**Richards S., Worley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.W.,

**Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

**Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Marking M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

**Richards M. Touchman J.W., Green E.D., Dickson M.C.,

**Richards M. Touchman J.W., Green E.D., Dickson M.C.,

**Richards M. Touchman J.W., Green E.D., Dickson M.C.,

**Richards M. I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

**Alones S.J., Marra M.A.,

**Jones S.J., Marra M.A.,

**Jones S.J., Marra M.A.,

**Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.;
                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.6%; Score 248; DB 2; Length 328; 38.3%; Pred. No. 1.5e-13; ive 22; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein S., Strausberg R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7938B5F56F9C58E7 CRC64;
                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS0017; DEATH DOWAIN; 1.
PROSITE; PS00652; THPR "NGFR 1; UNKNOWN_1.
PROSITE; PS50050; THPR "NGFR 2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL: BC074299; AAH74299.1; -...
GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004015; F:receptor activity: IEA.
GO; GO:000165; F:receptor activity: IEA.
GO; GO:0007165; F:receptor activity: IEA.
InterPro; IPR001450; 4Fe45 ferredoxin.
InterPro; IPR001029; Death.
InterPro; IPR001029; DEATH.
InterPro; IPR001029; DEATH.
InterPro; IPR001036; TNRR _G.
Pfam; PF00020; TNRR _G; I.
SWART; SM00005; DEATH; I.
  328 AA
                                                                                                                                               Kenopus laevis (African clawed frog)
                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 AA; 37262 MW;
                                       05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dev. Dyn. 225:384-391(2002)
  PRELIMINARY;
                                                                                                                                                                                                        Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                        XDR-M1 protein.
Name=XDR-M1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rissum=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiative.
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84 KCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRP 143
112 MVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTK-CPQGIPVLQECNSTANTVCSSSVS 170
                   98 EVRPCTATQNAECRCKKGTYCPMDHPCEVCLTCTESCPPGQSLHLPCNSTSDSHCGPAES 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 PCSPGTYTGLQNSLRKCLRCSTCSHNEEPKVACSTTSDVQCQCRQG-YYYDPE-SEMCFP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 LILLILLILLINDPLOVKFAMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCE
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;

Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;

"Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
                                                                                                                                                                                                                                                           nympnocystis disease virus - isolate China.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
NCB _TaxID=256729;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Carnivora; Fissipedia; Felidae; Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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InterPro; IPR06209; EGF like.
InterPro; IPR001366; TWRR c6.
Pfam; PF000200; TWRR c6; 2.
SWART; SM00208; TWRR; 4.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01086; TWRR_NGFR_1; UNKNOWN_2.
PROSITE; PS00500; TWRR_NGFR_2; 3.
Hypothetical protein.
SEQUENCE 289 AA; 32691 MW; 26B6114D4D5D6C3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q95185;
01-FRB-1997 (TrEMBLrel. 02, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
10-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumour necrosis factor receptor p60 (Fragment).
                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Lymphocystis disease virus - isolate China.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.8%; Score 239.5; DB 2
38.7%; Pred. No. 7.4e-13;
iive 13; Mismatches 49.
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                                                                                                                                                                               289 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | | : | | | CSNCESSKVKVTTCNRTHDTVC 117
                                                                                                                                                                                                                                                                                                                                                                                                                         78:6982-6994 (2004).
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nes 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                 PRELIMINARY;
                                                                                                 158 GSLKTWIW 165
                                                                  171 RRSASVAW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
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49; Conservative

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Local Similarity

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Name=xDR-M2
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 LLLLLLLLLLLLLLVPLQVKFAM----LELHSFKCPAGEY---WSKDVCCKNCSAGTFVKAPC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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WA WEDLINE=21455405; PubMed=11531421; DOI=10.1006/viro.2001.1042;
WA WEDLINE=21455405; PubMed=11531421; DOI=10.1006/viro.2001.1042;
WINF-alpha-induced cell death in feline immunodeficiency virus-
I'm forced cells is mediated by the caspase cascade.";
Virology 287.446.455(2001).
WE WEBL; AB051103; BAB55455.1; -.
WE REBL; AB051103; BAB55455.1; -.
WE GO; GO:0005515; F:protein binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000185; P:signal transduction; IEA.
RO; GO:000185; P:REPTO; P:RO0186; P:REPTO; P:RO0186; P:REPTO; P:RO0186; P:REPTO; P:RO0186; P:REPTO; P:REP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Carnivora, Fissipedia, Felidae, Felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.7%; Score 239; DB 2; Length 189; 35.3%; Pred. No. 5.5e-13; Live 19; Mismatches 70; Indels
Duthie S., Nasir L., Eckersall P.D.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor necrosis factor type I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 -YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 RYYWSETHFQCLNCSLCLNG-TVQISCKETQNTVCT 167
                                                                                                        GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR000345; CytC heme_BS.
InterPro; IPR001369; EGF Tike.
InterPro: IPR001369; TNFR_c6.
Pfam; PF00020; TNFR, c6, 3.
SMART; SW00208; TNFR; 3.
PROSITE; PS01190; CYTOCHROME C; UNKNOWN_1.
PROSITE; PS01186; EGF 2; UNKNOWN_1.
PROSITE; PS00652; TNFR_NGFR_1; 3.
PROSITE; PS50050; TNFR_NGFR_1; 3.
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                                                     EMBL; U72344; AAB95089.1; -. HSSP; P19438; 1EXT.
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                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
NON TER
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62 NCSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AGPGLDTDCRECENGTFTASENYIRQCLSCSKCRKEMYQVEISPCTVYRDTVCGCRKNQY 132
                                                                                                                                                                                                                                                                                                                                                                                                  74 EIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKD--QEMVADCSATSDRKCQCRTGLY 131
                                                                                                                                                                                                                                                                                                                           13 LVLÍALLVEIYPLRVTGLVPHLRDREKRAIPCPQGKÝIHPQDNSICCTKCHKGTYLYNDC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 FGFFS-----PELVVSTTNGLPLP------PEMYYQAGNIRCL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Pubmed-1466840; DOI=10.1074/jbc.M306217200;
Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
"Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLVRPAMLELHSFKCPAGEYWSKDVCCK
                                                                                                                                                                                                                                                        22 LLLLLLLLLLLLNPLQVKFAM----LELHSFKCPAGEY---WSKDVCCKNCSAGTFVKAPC
                                                                                                                                                                                     12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                    Query Match 23.1%; Score 233; DB 2; Length 446; Best Local Similarity 34.6%; Pred. No. 4e-12; Matches 54; Conservative 19; Mismatches 71; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Indels
PROSITE; PS50050; TNFR NGFR 2; 3.
SEQUENCE 446 AA; 49563 MW; 217BD331DD8A74AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 AA; 36586 MW; 3FCD1CCAB8533355 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q76B98;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 -YYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCS 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    differential mechanisms.";

differential mechanisms.";

Dial. Chem. 279:7629-7635 (2004).

EMBL; ABIL147; BAD1171.1;

GO; GO:0005515; F:procein binding; IEA.

GO; GO:0007165; P:signal transduction; IEA.

GO; GO:0007165; P:signal transduction; IEA.

InterPro; IPR001489; Death.

InterPro; IPR001489; Death.

InterPro; IPR0011029; DEATH like.

InterPro; IPR001369; TNFR_GG.

Pfam; PF00209; TNFR_Gf.

Pfam; PF00209; TNFR_Gf.

SMART; SM00206; DRATH; 1.

SMART; SM00206; DRATH; 1.

PROSITE; PS500199; 4FR4S PERREDOXIN; UNKNOWN_I.

PROSITE; PS500191; DEATH—DOMAIN; 1.

PROSITE; PS000191; TNFR_GRE.

PROSITE; PS000502; TNFR_NGFR_1; UNKNOWN_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 23.0%; Score 232; DB 2; Local Similarity 32.7%; Pred. No. 3.7e-12; tes 56; Conservative 22; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopodinae; Xenopus
NCBL_TaxID=8355;
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Search completed: September 9, 2005, 09:19:10 Job time : 672.857 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

8, 2005, 17:05:32 September е С Run

2; Search time 544.286 Seconds (without alignments) 127.905 Million cell updates/sec

US-10-622-407-10

Perfect score:

1008 1 MFGFFCSLVSSLSRWFLWRR......ANTVCSSSVSRRSASVAWPI 180 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:*

geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	de				
Score	Query Match	Length	DB	ID	Description
1008	100.0	180	_	ABW02716	Abw02716 Mouse tms
1008	100.0	180	8	ADJ45754	Adj45754 Murine tm
926	94.8		7	ABW02715	Abw02715 Mouse tms
926	94.8	-	œ	ADJ45752	
926	94.8	398	7	ABW02717	Abw02717 Mouse tms
926	94.8	398	œ	ADJ45758	Adj45758 Murine tm
748	74.2	133	7	ABW02714	Abw02714 Mouse tms
748	74.2	133	œ	ADJ45750	_
709	70.3	396	6 0	ADF57557	Adf57557 Mouse ymk
705	69.9	176	~	AAW80254	Aaw80254 Amino aci
705	69.9	176	80	ADF57551	Adf57551 Mouse ymk
705	6.69	176	60	ADM46623	Adm46623 Mouse 7F4
641	63.6		œ	ADM46624	Adm46624 Mouse 7F4
542.5	53.8	380	4	ABG09344	Abg09344 Novel hum
467	46.3		œ	ADF57549	
299	29.7	204	ı	ABB81467	Abb81467 Murine TA
217.5	21.6		ω	ADF57553	Adf57553 Mouse TNF
217.5	21.6		Ŋ	AA022289	Aao22289 TNFR1 exp
217.5	21.6		œ	ADT08167	Adt08167 Murine tu
208.5	20.7	355	N	AAR85073	Aar85073 Cowpox vi
208.5	20.7		4	AAB50524	Aab50524 Human tum
208.5	20.7		80	ADJ96165	Adj96165 Human CRM
207.5	20.6	28	~	AAW33359	Aaw33359. TBP (20-19
205	20.3	350	Ŋ	ABB81468	Abb81468 Viral Crm
204.5	20.3	461	7	ADE57927	Ade57927 Rat Prote

MICH COMMITTER CONTRACTOR	Adr90160 Human tum Aab66979 Tnfrl pro Adm28817 TNFR supe Adr90161 Human tum
ADQ76809 AAW33358 AAW33358 AAW33360 ABC74754 AAR07450 AAR07450 AAR0759 AAR24080 AAR24080 AAR24080 AAR99225 AAR99225 AAR990162 ADR90162	ADR90160 AAB66979 ADM28817 ADR90161
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204 204 203 203 203 203 201 201 201 201 501 501 501 501 501 501 501 501 501 5	201 201 201 201
22222222222222222222222222222222222222	4 4 4 4 2 6 4 0

ALIGNMENTS

ABW02716 standard; protein; 180 AA (first entry) 11-MAR-2004 ABW02716; **ABW0271**

Mouse tmst2-receptor splice variant protein.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse; splice variant

Mus musculus

US6627199-B1.

30-SEP-2003.

07-JUL-2000; 2000US-00612033

99US-0143063P 09-JUL-1999;

(AMGE-) AMGEN INC.

Saris C;

WPI; 2003-874309/81. N-PSDB; AAD64755 New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping

Claim 1; SEQ ID NO 10; Opp; English.

The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome

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                                                                                                                                                                                                                                                                                                                                                                                                                                          DRKCQCRTGLYYYDDKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSASVAWFI 180
                                                                                                                                                                                                                                                                                                                                             KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSASVAWPI 180
                                                                                                                                                                                                                                                1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCC 60
                                                                                                                                                                                                                                                                            1 MFGFFCSLVSSLSRWFLWRRLLILLILLILLILLILLILLOVKFAMLELHSFKCPAGEYWSKDVCC 60
identification or mapping. The invention is useful in gene therapy. The present sequence is mouse tmst2-receptor splice variant protein used in the exemplification of the invention
                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   ö
                                                                                                                                                 Length 180;
                                                                                                                                                                                                 Indels
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Pred. No. 2e-75;
                                                                                                                                                 DB 7;
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                                                                                                                                                   100.0%;
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                                                                                                                                                                          Local Similarity
                                                                                                    Sequence 180 AA;
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                                                                                                                                                   Query Match
                                                                                                                                                                                                 Matches
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Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; autoimmune disease; cachexia; cancer; cerebral malaria; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid archiritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease; Murine tmst2-receptor splice variant polypeptide. tmst2-receptor splice variant; receptor. ADJ45754 standard; protein; 180 AA (first entry) 06-MAY-2004 ADJ45754; RESULT 2 ADJ45754

Mus musculus.

US2004018544-A1.

29-JAN-2004.

17-JUL-2003; 2003US-00622407

09-JUL-1999; 99US-0143063P.

(SARI/) SARIS C.

Saris C;

2004-224390/21. WPI; 2004-224390/ N-PSDB; ADJ45753. Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.

Claim 13; SEQ ID NO 10; 57pp; English.

polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, carebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia, lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ The invention relates to a tmst2-receptor polypeptides and the

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                                                                                                                                                                                                                                                                                                             61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                  DRKCQCRTGLYYYDPKPPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSASVAWPI 180
rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-receptor splice variant polypeptide of the invention.
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                                                                                                                                                                                                                 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                  1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                        KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS
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                                                                                                                                                                            Gaps
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0
                                                                                                                                        Length 180;
                                                                                                                                                                            Indels
                                                                                                                                      ; Score 1008; DB 8;
; Pred. No. 2e-75;
0; Mismatches 0;
                                                                                                                                          100.08;
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                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 180; Conservative
                                                                                                     180 AA;
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RESULT 3

ABW02715 standard; protein; 198 AA.

ABW02715;

(first entry) 11-MAR-2004 Mouse tmst2-receptor protein.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory; disease; chromosome mapphing; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunosupdator; antilnflammatory; antiparasitic; cytostatic; mouse.

Mus

US6627199-B1.

30-SEP-2003

07-JUL-2000; 2000US-00612033.

99US-0143063P. 09-JUL-1999;

(AMGE-) AMGEN INC.

Saris C;

WPI; 2003-874309/81. N-PSDB; AAD64754. New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for chromosome mapping

Claim 1; SEQ ID NO 8; Opp; English.

The invention relates to transmembrane decoy-receptor (tmst2) proteins and their secreted splice variants, belonging to the tumour necrosis factor (TMF) receptor super gene family and polymucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome identification or mapping. The invention is useful in gene therapy. The

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invention.
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                                                                   Query Match
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                                                                                                                                                                                                                                                               RESULT 5
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                                                                                                                                                              KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                               Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                              KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                    9
                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
                                                                                                                1 MFGFPCSLVSSLSRWFLWRRLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                             Gaps
                                                                                                                                                                                            DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
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present sequence is mouse tmst2-receptor protein used in the exemplification of the invention
                                                       94.8%; Score 956; DB 7; Length 198;
                                                                             0; Indels
                                                                    4.4e-71;
                                                               100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claim 13; SEQ ID NO 8; 57pp; English.
                                                                                                                                                                                                                                                                          ADJ45752 standard; protein; 198 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JUL-1999; 99US-0143063P. 07-JUL-2000; 2000US-00612033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003; 2003US-00622407
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                             Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                              Murine tmst2-receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-224390/21.
                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADJ45751
                                  Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2004018544-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SARI/) SARIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                       06-MAY-2004
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                                                                                                                                                                                                                                                     RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cachexia; autoimmune disease; inflammatory disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic; cytostatic; mouse; human; immunoglobulin Fc region; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
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                                                                                                                                                                                                                                                                                                                                                                                1 MPGPFCSLVSSLSRWFLWRRLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLDDQVKFAMLELHSFKCPAGEYWSKDVCC
distress syndrome (ARDS), tuberculosis and a number of viral diseases This sequence represents the murine tmst2-receptor polypeptide of the
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
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                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                               Score 956; DB 8; I
Pred. No. 4.4e-71;
                                                                                                                                                                                                                                                                   Best Local Similarity 100.0%; Pred. No. 4.4 Matches 170; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 14; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABW02717 standard; protein; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUL-2000; 2000US-00612033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0143063P
                                                                                                                                                                                                                                   94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Mus musculus
Chimeric - Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-874309/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD64758
                                                                                                                                                                Sequence 198 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autodimmune disease; acabexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia; phyphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                       KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                KNCSAGIFVKAPCEIPHIQGQCEKCHPGIFIEKDNYLDACILCSTCDKDQEMVADCSAIS 120
present sequence is a fusion protein comprising mouse tmst2- receptor protein and human immunoglobulin Fc region. This sequence is used in the exemplification of the invention
                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.
                                                                                                                                  1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLDPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                          DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                        ..
0
                                                                               Length 398;
                                                                                                        Indels
                                                                                                          .
0
                                                                                            Pred. No. 8.8e-71;
                                                                               DB 7;
                                                                                      100.0%; Preu. ...
                                                                               Score 956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 14; 57pp; English.
                                                                                                                                                                                                                                                                                                                                   ADJ45758 standard; protein; 398 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tmst2-Fc fusion protein; receptor
                                                                                                                                                                                                                                                                                                                                                                                                                 Murine tmst2-Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2003; 2003US-00622407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0143063P.
2000US-00612033.
                                                                               94.88;
                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                        170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-224390/21.
N-PSDB; ADJ45757.
                                                                                            Similarity
                                                     Sequence 398 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2004018544-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SARI/) SARIS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-1999;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                        06-MAY-2004
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                                                                               Query Match
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                                                                                             Local
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The invention relates to a tmst2-receptor polypeptides and the polymuclectide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, and diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation,

mālaria, diabetes mellitus, disseminated intravascular coagulatiou, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and their secreted splice variants, belonging to the tumour necrosis factor (TNF) receptor super gene family and polynucleotides encoding such proteins. The composition and methods are useful in diagnosing, treating or ameliorating diseases associated with or resulting from abnormal tmst2 and/or abnormal expression of its putative ligand, such as sepsis, cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial and parasitic diseases or cancer. They may also be used for chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis; cachexia; autoimmune disease; inflammatory; disease; chromosome mapping; cancer; chromosome identification; gene therapy; antibacterial; virucide; immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
                                                                                                                                                                                                                                                                                        KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                          KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
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                    respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to transmembrane decoy-receptor (tmst2) proteins
lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respliatox distress syndrome (ARDS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-Fc fusion protein of the
                                                                                                                                                                                                                   1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                     1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLVRPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tmst2 nucleic acid molecule and polypeptide, useful for diagnos ating or ameliorating diseases associated with or resulting from ormal tmst2 expression, e.g. sepsis, inflammation or cancer, or
                                                                                                                                                                                                                                                                                                                                                                  DRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                     DRKCOCKTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                 ö
                                                                                                                                           Length 398;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse tmst2-receptor protein from tmst2-00004-d1 clone.
                                                                                                                                                                                   .
0
                                                                                                                                           94.8%; Score 956; DB 8; 1
100.0%; Pred. No. 8.8e-71;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 6; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABW02714 standard; protein; 133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUL-2000; 2000US-00612033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-874309/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAD64753.
                                                                                                             Sequence 398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus
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                                                                         invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABW02714;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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Mus musculus.
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                                                                                                                                                                                                              Matches 133;
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                                                                                          invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a tmst2-receptor polypeptides and the polynucleotide encoding them. The sequences of the invention are useful for treating diseases and conditions including acquired immunodeficiency syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral malaria, diabetes mellitus, disseminated intravascular coagulation, haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
                                                                                                                                                                                                                                                                                                 KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                          KNCSAGTFVKAPCEIPHTOGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                        9
    gene therapy. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel tmst2-receptor polypeptide useful for diagnosing and treating disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; tmst2-receptor; tmst2 00004-d1; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis;
                                                                                                                                                                                                                1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLDPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                           MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLNLPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection;
                        in the
                                                                                                                             Length 133;
                                                                                                                                                                    Indels
identification or mapping. The invention is useful in present sequence is mouse tmst2-receptor protein used exemplification of the invention
                                                                                                                             DB 7; L
4.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rheumatoid arthritis; septic shock; stroke;
                                                                                                                          74.2%; Score 748; DB
100.0%; Pred. No. 4.4
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; SEQ ID NO 6; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADJ45750 standard; protein; 133 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine tmst2 00004-d1 polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                     DRKCQCRTGLYYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                          DRKCOCRTGLYYY 133
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                                                                                                                                              Local Similarry
nes 133; Conservative
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                                                                                     Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.
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                                                                                                                               Query Match
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                                                                                                                                                                      Matches
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lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory distress syndrome (KADS), tuberculosis and a number of viral diseases. This sequence represents a murine tmst2-receptor polypeptide clone of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; cancer; acquired immune deficiency syndrome; ALDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLDPLQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel ymkz5-receptor polypeptide useful for treating diseases such as tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MFGFFCSLVSSLSRWPLWRRLILLLLLLLLLLLLDQVKFAMLELHSFKCPAGEYWSKDVCC
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                       Length 133;
                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                       74.2%; Score 748; DB 8; L
100.0%; Pred. No. 4.4e-54;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 4; SEQ ID NO 14; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse ymkz5-human Fc fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF57557 standard; protein; 396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2002; 2002US-00193616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999; 99US-0143137P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRKCQCRTGLYYY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DRKCÓCRIGLYNY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-008943/01.
                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                       Sequence 133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZHAN/) ZHANG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003096355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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Sequence 176 AA;

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cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymkz5-human Fc fusion protein.
                                                                                                                                                                                                                        67 TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.
                                                                                                                                                                                        26
                                                                                                                                                                                                                                            57 TFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC
                                                                                                                                                            7 SLVSSLSRWFLWRRLLLLLLLLLLLLLLLLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                          -----LLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor protein inducing differentiation in osteoblast cells - has extracellular region only and can be used for screening substances f treatment of bone growth disorders.
                                                                                                                             8
                                                                                                                                                                                                                                                                                                          SIGLYYYDPKFPESCRPCTKCPQGIPVLOECNSTANTVCSSSVSNAAA 164
                                                                                                                                                                                                                                                                                      127 RIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVSRRSA 174
                                                                                            Length 396;
                                                                                                                             22; Indels
                                                                                            Score 709; DB 8;
Pred. No. 2.2e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
                                                                                                                           6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29. .176
/note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .. .28
'note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 29-31; 51pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of protein 7F4.
                                                                                                                                                                                                                                                                                                                                                                                                     AAW80254 standard; protein; 176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-JP001511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97JP-00099653
                                                                                              70.3%;
78.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                             Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toyoshima T;
                                                                                                                                                                                          SHVSSLSHWF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-568275/48.
                                                                                                            Local Similarity
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                                                              Sequence 396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9843998-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-OCT-1998
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                                                                                                                                                                                          Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW80254;
                                                                                                                                                                                                                                                                                                                    117
                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
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The invention relates to transmembrane decoy receptor, ymkz5 belonging to tumour necrosis factor (TNF) receptor supergene family and nucleic acid sequences encoding such receptors. The invention is useful for detecting diseases or susceptibility to diseases related to the presence of mutated ymkz5-receptor gene such as tumours or cancers. The sequences of the invention are used as medication for a number of diseases such as acquired immune deficiency syndrome (AIDS), anaemia, auchimune diseases, cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial ischaemia, obesity etc. The invention is also useful in gene therapy. The present sequence is mouse ymkz5 receptor protein.
                               ï
                                                                                                                                                 TFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLHDCELCSTCDKDQNNVADCSATSDRKCEC 116
                                                                                                                           TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; cancer; acquired immune deficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                               99
                                                                                             99
                                                                                7 SLVSSLSRWFLWRRLLLLLLLLLLLLLDPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel ymkz5-receptor polypeptide useful for treating diseases such asttumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                               8;
Length 176;
                                                                                                                                                                                                              127 RIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                               Indels
                               20;
Score 705; DB 2;
Pred. No. 2.1e-50;
                              5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; SEQ ID NO 8; 57pp; English.
                                                                                                                                                                                                                                                                                                        ADF57551 standard; protein; 176 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-2002; 2002US-00193616.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-1999; 99US-0143137P.
69.9%;
                79.98;
                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      Mouse ymkz5 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-008943/01.
N-PSDB; ADF57550.
                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ZHAN/) ZHANG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US2003096355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                  Best Local Simi
Matches 131;
                                                                                                                                                                                                                                                                                                                                                                        12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-2003
                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                          ADF57551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor.
 Query Match
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DB 8; Length 176;

69.9%; Score 705;

Query Match

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Novel human diagnostic protein #9335
                                                                                                                                         Mouse 7F4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 148 AA;
                                                                                                                                                                                                                         WO2004026026-A1
                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-FBB-2002
                                                                                                                   17-JUN-2004
                                                                                                                                                                                                                                                 01-APR-2004
                                                                                            ADM46624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG09344;
                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
             셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a transgenic non-human animal having the expression of 7F4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agents for the prevention and treatment of diseases including osteoporosis, obesity and diabetes. The present sequence represents the modified mouse 7F4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                TPVKAPCEIPHTQGQCEKCHPGTPTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHVSSLSHWF-----LLLLLLLLLLFVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG 56
                                                         26
                                                                                               TFVKAPCKI PHTQGQCEKCHPGTPTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC
                                                  SHVSSLSHWF-----LLLLLLLNLFLPVIFAMPESYSFNCPDGEYQSNDVCCKTCPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVSSLSRWFLWRRLLLLLLLLLLLLLLVPLQVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                    SLVSSLSRWFLWRRLLLLLLLLLLLLLLLOVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transgenic non-human animal with modified expression of 7F4 gene for screening remedies for bone or glycolipid metabolism disorders.
                                                                                                                                                                                                                                                                                                         7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8; Length 176;
                                                                                                                                           127 RTGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                             RIGLYYYDPKFPESCRPCTKCPQGIPVLQECNSTANTVCSSSVS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
             Indels
            20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.9%; Score 705; DB 8; 79.9%; Pred. No. 2.1e-50; iive 5; Mismatches 20;
  Pred. No. 2.1e-50;
             5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; SEQ ID NO 2; 44pp; Japanese.
                                                                                                                                                                                                              ADM46623 standard; protein; 176
                                                                                                                                                                                                                                                                                                                                                                                                                 10-SEP-2003; 2003WO-JP011545.
                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002; 2002JP-00270321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saito H, Makishima
  79.98;
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHUS ) CHUGAI SEIYAKU KK.
             Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 79.8
Matches 131; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-340227/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
  Best Local Similarity
                                                                                                                                                                                                                                                                                  Mouse 7F4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ADM46622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 176 AA;
                                                                                                                                                                                                                                                                                                                                                                    WO2004026026-A1.
                                                                                                                                                                                                                                                                                                                                              Mus musculus.
                                                                                                                                                                                                                                                            17-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                          01-APR-2004.
                                                                                67
                                                                                                      57
                                                                                                                              127
                                                                                                                                                                                                                                     ADM46623;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kake T,
                                                                                                                                                                                       RESULT 12
ADM46623
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The present invention relates to a transgenic non-human animal having the expression of 7F4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agents for the prevention and treatment of diseases including osteoporosis, obesity and diabetes. The present sequence represents the modified mouse 7F4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99 ACILCSTCDKDQEMVADCSATSDRKCQCRTGLYYYDPKFPESCRPCTKCPQGIPVLQECN 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DCELCSTCDKDQNMVADCSATSDRKCECQIGLYYYDPKFPESCRPCTKCPQGIPVLQECN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AMPESYSFNCPDGEYQSNDVCCKTCPSGTFVKAPCKIPHTQGQCEKCHPGTFTGKDNGLH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AMLELHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression of 7F4 gene for metabolism disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes.
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Pred. No. 3.3e-45;
5; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic non-human animal with modified screening remedies for bone or glycolipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; SEQ ID NO 3; 44pp; Japanese.
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ADM46624 standard; protein; 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kake T, Saito H, Makishima F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-SEP-2003; 2003WO-JP011545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2002; 2002JP-00270321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 63.6%;
Best Local Similarity 84.8%;
Matches 112; Conservative
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynuclectides are also used in diagnostics as expressed sequence tags for identifying expressed sectivity of (II) as useful in gene therapy techniques to restore normal crivity of (II) as useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, formsics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at (ftp.wipo.int/pub/published_pot_esequences)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 LHSFKCPAGEYWSKDVCCKNCSAGTFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACIL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 LVSSLSRWFLWRRLLLLLLLLLLLLNLPLQ-------VKFAMLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess blodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
               Human; chromosome mapping; gene mapping; gene therapy; forensic
food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53.8%; Score 542.5; DB 4; Length 380; 80.2%; Pred. No. 1.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; SEQ ID NO 39703; 103pp; English.
                                                                                                                                                                                    10-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                      2000US-00540217
2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                        2001-639362/73.
                                                                                                                                                                                                                                                                                                                   Ormanac RT, Liu C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSTCDK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 380 AA;
                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS73531
                                                                                                          WO200175067-A2
                                                                                                                                                                                                                        31-MAR-2000;
                                                                         Homo sapiens
                                                                                                                                                                                                                                          23-AUG-2000;
                                                                                                                                               11-OCT-2001.
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ADF57549 standard; protein; 117 AA.

ADF57549 ID ADF5

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57 TFVKAPCKIPHTQGQCEKCHPGTPTGKDNGLHDCELCSTCDKDQNMVADCSATSDRKCEC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TFVKAPCEIPHTQGQCEKCHPGTFTEKDNYLDACILCSTCDKDQEMVADCSATSDRKCQC 126
                                                                                                                     Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour; cancer; acquired immune deficiency syndrome; ALDS; anaemia; autoimmune disease; cachoxia; leprosy; leukaemia; hepatitis; multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHVSSLSHWF-----LLLLLLLLLPVIFAMPESYSFNCPDGEYOSNDVCCKTCPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel ymkz5-receptor polypeptide useful for treating diseases such as tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy, leukemia, hepatitis, multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLVSSLSRWFLWRRLLLLLLLLLLLLLOVKFAMLELHSFKCPAGEYWSKDVCCKNCSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19; Indels
                                                                                       Mouse ymkz5 receptor from clone ymkz5-00013-g11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 46.3%; Score 467; DB 8; Local Similarity 73.6%; Pred. No. 6.1e-31; les 89; Conservative 5; Mismatches 19;
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                                                                                                                                                                                                                                                                                                                                            11-JUL-2002; 2002US-00193616.
                                                                                                                                                                                                                                                                                                                                                                           09-JUL-1999; 99US-0143137P. 07-JUL-2000; 2000US-00611989.
                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117 AA;
                                                                                                                                                                                                                                                                     US2003096355-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                (ZHAN/) ZHANG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 R 127
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                                                                                                                                                                                                                                   Mus musculus.
                                                    12-FEB-2004
                                                                                                                                                                                                                                                                                                        22-MAY-2003
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                  ADF57549;
                                                                                                                                                                                                receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhang K;
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Matches
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